

FIGURE 1

CCAATGCCCGGTGCGGTGGTGCAGGGCTCGGGCTAGTC**ATG**GCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTCAGAGAGCGTTCTGCTAATCTACACTTTATTTTC
TGGATCACTGGCGTTATCCTTCTGCAAGGGCTTGAGCTTGGGAGGCTGGAGAATTA
CTTTCTCTTAAATGAGAAGGCCACCAATGTCCCCTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTGGGCACCTTGGTTGTTGCTACCTGCCAGCCTGATGGATGCTA
AAACTGTATGCAATGTTCTGACTCTCGTTGGTCGAACCTGGCGCTGCCATCGTAGG
ATTTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTGTTGGTGTCAACCGATTATAGAGATTGGACAGATACTAATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAACCTGAAAGATTGACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTCCTTGGAGTTGCTTCCAACTGATTGGAATCTTCTGCCACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTGT**TAA**CCCAATGTATCTGTGGCCTATTCCCT
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTGGCTGGAGAACTG
ACAACACTACTGATAGACCAAAAAACTACACCAAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTGCTATGTTCAAGTCCACCTCTATCCCATTGTTAGATCG
TTGAAACCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

FIGURE 2

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><MW: -1, pi: 8.36, NX(S/T): 1
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VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAlTNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACCGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTGCCGTTCTCGGACCTGTACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCGGAGGGTAGAGAAAGTCAGT
GCCACAGCCCCGACCAGCGCTGCTCTGAGCCCTGGCACGCCAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGAAACAGCCGCTCGAGCCTGGGCCGGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCGGAGAGAGGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTCCACCGAGGCCGCGCTTGAGGGATCTGAAGAGGTTCCCTAGAACAGGGT
GTTCCCTCTTCGGGGTCCTCACAGAACAGGTTCTGGGGTCGCCCTCTGAGGAGGCT
GCGGCTAACAGGGCCAGAACCTGCCATTGGATGTCCAGAACCTCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTCTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTCC
TCAACTCCAGGTTATGAAAACAGTACTTGGAAAAGTACCTAA**ATG**ATCGTCTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAACGCCCTGGCCAGGGTCTGTTGACTCTCGAAGAG
CACATAGCCCACCTCCTAGGGACTGGAGGTGCCGCTACTACCAGGGTAATTCCGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
CACTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCCTGTTGCCACCAAGGAGGGC
CGAGGACCTCATGAGCCAAGGGAGAAAAGAACAAAATGTGGATGGCTAGTGTGGACACACT
GGCAGTAATAACGGACTCTGTAGATAAG**TAA**GTATCTGACTCACGGTCACCTCCAGTGGAAAT
GAAAAGTGTCTGCCGGAACCATGACTTTAGGACTCCTCAGTCCCTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAAATTAAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTGATGTTTGCTGCTGTCATCTACTTGTCTGGAAATGTCTAAATGTTCTG
TGTAGCAGAAAACACGATAAAGCTATGATCTTATTAAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCCTGTCCACCGGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTGGCC
CCGACGCCCTGTCTCGGAATCAGGGTGCCTGCAGATTGAGGTCCCAGTTCTAACGGACTG
CAAGATGGAGGAAGGCAGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGCATGCAAATGTGGGTGACCTCGTCTCAGGCTTCCTGCTTTCCGAAGC
CTTCCCCGACATACCTCGGACTAGTGCAGAGCAAACCTTCCCCTACTTCCACATCTC
CATGGGCTGTGCCCTCATCAACCTCTGCATCTGGCTTCACAGCATGCTGGCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTACCTGCTGTTCTGAGCCTACGCTGGCACTGTCAAC
GCCCGCTGGCTGGAACCCGACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGTCCCACCCCTACCGCCAGCTGC
GAGAGAAGGACCCAAGTACAGTGCCTCCGCCAGAAATTCTCCGCTACCATGGCTGTCC
TCTCTTGCAATCTGGCTGCGTCCTGAGCAATGGCTCTGCTCGCTGGCCTGCCCTGGA
AATAAGGAGCCTCT**TAG**CATGGGCCCTGCATGCTAATAATGCTTCTCAGAAATGAAAAAAA
AAAAAAAAAAA

FIGURE 6

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GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVL SNGLCLAGL ALEIRSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAAGATTTAAGCCCATTCTGCAGTGGAAATTGATGAACTAGCAAGAGGACACCCTT
CTTGTATTATAACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTTTGGGT
GCTAGGCCTCCTAATCCTCTGTGGTTCTGTGGACTCGTAAAGGAAAACATAAGATTGAAG
ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGAAACTTGGCAGCC
AGAACCTTGATAAAAAGGGATTCATGTAATCGCTGCCGTGACTGAATCAGGATCAAC
AGCTTAAAGGCAGAACCTCAGAGAGACTCGTACTGTGCTTCTGGATGTGACCGACCCAG
AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGT
CTGATCAATAATGCTGGTGTCCCGCGTGTGGCTCCACTGACTGGCTGACACTAGAGGA
CTACAGAGAACCTATTGAAGTGAACCTGTTGGACTCATCAGTGTGACACTAAATATGCTTC
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAAATGTCCTCAGTGGAGGTGCCCTGCA
ATCGTGGAGGGGCTATACTCCATCAAATATGCACTGGAAAGGTTCAATGACAGCTTAAG
ACGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
ACTTGGCAGATCCAGTAAAGTAATTGAAAAAAACTGCCATTGGAGCAGCTGTCTCCA
GACATCAAACAACATATGGAGAAGGTTACATTGAAAAAAAGTCTAGACAAACTGAAAGGCAA
TAAATCCTATGTGAACATGGACCTCTCCGGTAGAGTGCATGGACCACGCTCTAACAA
GTCTCTCCCTAAGACTCATTATGCCGTGGAAAAGATGCCAAATTCTGGATACCTCTG
TCTCACATGCCAGCTTGCAAGACTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
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TTCAAGAACACATCTCCTTTCAACCCATTCTTATCTGCTCCAACCTGGACTCATTTAGA
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FIGURE 8

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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSSLRDMKAFGVHVSCIEPGLFKTNLADPVKIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATGG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCCTGACGCCGAGTGGCGGGGCCCTTGGCCGTGCCACCACT
 GTAGTCATGTACCCACGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCCGCTCGTGTGGAGGAAATGGA
 AGCAACTGTGAGATTGCAGCGGAATATGATTCTCTCCTGCCTTCTGCTTTCTGT
 GGACTCCTCTTACATCAACTGGCTGACCATTGAAAGCTCTGGCTTCAGGCTAGAGGA
 AGAGCAGAACATGAGGCCAGAAATTGCTGGTTAAAACCAGCAAATCCACCGTCTTACCAAG
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 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
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 CTCCCTCAAGAACAGAGCAGAACTGCCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG
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 GAGTGGTTGGCCTCGGTCTCACACTGATCGACGCCCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCAGAAGAAGTTACACTTTGAAAAGGACG
 TGGACGTCAACCTGTTGAGAGCACGATCCGCATCCTGGGGGGCTCTGAGTGCCTACAC
 CTGTCTGGGACAGCCTTCCTGAGGAAAGCTGAGGATTGGAAATCGGCTAATGCCTGC
 CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC
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 GAGCTCTCCGTCACAGGGATAAGAAGTTCAGGAGGCAGTGGAGAAGGTGACACAGCA
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 AGCCATCGAGGGTGTCAAACGCACCTGCTGCCACTCGGAGGCCAGTAAGCTCACCTTG
 TGGGGAGCTGCCACGGCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCCTGCCA
 GGGACGCTGGCTCTGGCGTCTACCACGGCCTGCCGCCAGCCACATGGAGCTGGCCAGGA
 GCTCATGGAGACTTGTACAGATGAACCGCAGATGGAGACGGGCTGAGTCCCAGATCG
 TGCACCTAACCTTACCCCAGCCGGCGTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTGCCAGAGACCGTGGAGAGCCTGTTCTACCTGACCGCTCACAGGGGA
 CCGCAAATACCAAGGACTGGGCTGGAGATTCTGAGGCTTCAGCCGATTCACACGGGTCC
 CCTCGGGTGGCTATTCTCCATCAACAATGTCAGGATCCTCAGAAGGCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTCTGGGGAGACGCTCAAGTATCTGTTCTGCTCTCCGATGA
 CCCAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCCCTGCCTATCT
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGACTTCGGGTGGCAGAGGCACCTTG
 CTGGGTCTGGCATTTCAGGGCCACGTAGCACCGCAACCGCCAAGTGGCCAGGCT
 CTGAACCTGGCTCTGGCTCCTCGTCTCGTTAATCAGGACACCGTGAGGACAAGTGA
 GCCGTCAGTCTGGTGTGATGCCGGTGGCTGGCGCTGGAGCCTCCGCTGCTTCCTC
 CAGAACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTTGGCCGACCA
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 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTGTTACAAGCTGGACTCAGGGATCCTC
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FIGURE 10

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IAGLK PANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPLQIRPPSQDLKDGTQEET
KRQEAPVDPDRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVPTKPPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEAA
RKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTL GARADSYYEYLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYQPGRDVEVKPADRHNLLRPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCGGAGGCCGGCCGGCTGCGAGCGCCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGGCCAGCTGCCCTGGGAGGAACGGC
 AGGTCCGGGTTGCTCTCCGGCGGCCCTCCCTCGGAAGTGTTCGTCTCCACCTGTTGTGGC
 CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
 CCCGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCTGGCAGAG
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
 GCCCTCCGCGAACGCTTCGAGGAGCTCCTGGTCTCGTGCCTCACATGCGCCGCTTCCTGA
 GCAGGAAGAAGATCCGGCACCATCTACGTGCTAACCAAGGTGGACCACTTCAGGTTAAC
 CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTCCTGAGGCTGGC
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTTACCACTACAAGACCTATGTCGGCGGC
 ATCCTGCTGCTCTCCAAGCAGCACTACCGCTGTGCAATGGATGTCCAACCGCTTGTGGG
 CTGGGGCCGCGAGGACGACGAGTTCTACCGCGCATTAGGGAGCTGGCTCCAGCTTTCC
 GCCCCTCGGAATCACAACTGGGTACAAGACATTCGCCACCTGCATGACCCAGCCTGGCG
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 AGGCCTGAACACTGTGAAGTACCATGTGGCTCCCGCACTGCCCTGTCTGTGGCGGGGCC
 CCTGCACTGTCCCTAACATCATGTTGACTGTGACAAGACGCCACACCCTGGTGCACATT
 AGC**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATTGCTCAGGCTCAGGA
 CAAGGCCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
 AGCTACGCAATTGCAGCCACCCGGCGCCAAGGCAGGCTGGCTGGCCAGGACACGTGGG
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FIGURE 12

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RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDILLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDDEFYRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEKFVDRREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGGCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTAAAGGCTCATGCTGGAGTGGGACTGGTCGGTGCCCAGAAAGTCT
CTTCTGCCACTGACGCCCATCAGGGATTGGCCTTCTTCCCCCTCCTTCTGTGTCTC
CTGCCTCATCGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT
GGGGATGGCTAAGAAAGCTGGAGATAGGAACAGAAAGAGGGTAGTGGTGGCTAGGGG
GCTGCCTTATTAAAGTGGTTGTTATGATTCTTACTAATTATAAAAGATATTAAGGC
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FIGURE 14

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PRGEGEKVGDG
```

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

Sequence

GGGACCCATGCGGCCGTGACCCCCGGCTCCTAGAGGGCCCAGCGCAGCCGCAGCGGACAAAG
 GAGCATGTCCCGCGCCGGGAAGGCCCCTCCGGCCGATAAGGCTCCGGTCGCCGCTGG
 GCCCGCGCCGCGCTCTGCCCAGGGCTCCGGGGCGGCCGCTAGGCCAGTGCGCCGCC
 CTCGCCCCGCAGGCCGGCCGCAGC**ATG**GAGCCACCCGGACGCCGGCGGGGCCGCGCA
 GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCCTGCTGGGAGGCAGGCC
 CGGGCGGCCGCCGGCTGCCGGCTGCAAGCACGATGGCGGCCCGAGGGGCTGG
 AGGGCGGCCGCCGGCGAGGGCAAGGTGGTGTGAGCAGCTGGAACTCGGCAGGTCC
 GCCCCCAGATACTCTGCCAACCGCACGGTACCCCTGATTCTGAGTAACAATAAGATATCC
 AGCTGAAGAATGGCTCATTCTGGGTTAAGTCTCCTGAAAGATTGGACCTCGAAACAAT
 CTTATTAGTAGTATAGATCCAGGTGCCTCTGGGACTGTCATCTAAAAAGATTGGATCT
 GACAAACAATCGAATAGGATGTCGAATGCAGACATATTGAGGACTCACCAATCTGGTTC
 GGCTAAACCTTCGGGGATTGTTCTCATTATCTCAAGGAATTGATTATCTTGCG
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 GAATTGCCGTCTTCTACATGACTCCATCTCATGCCAACGTTGTGTTGAAGGAGACAGCCT
 TCCTTCCAGTGCATGGCTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAGGATG
 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTGTTGAAAAGAACATGATTACAAC
 TGCTCCTGATTGCAAGTGCCTAACCAATTCTAATATTCAAGGCTGGATCTACTGGAAATTG
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 ACTTCGGATTATGGGAGGGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTAAAGT
 GCAATGTTCAAATACATTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATT
 AAGACTATTACAGT**TAA**ATTAGAATGCTCAAATGTTCTGCTCGAAAATAACCTTATTA
 AAAGATTTTTGCAGGAAGATAGGTATTGCTTTGCTACTGTTAAAGAAAACA
 ACCAGGAAGAACTGCATTACGACTTCAAGGGCCCTAGGCATTGGCTTGATTCCCTT
 CTTCACATAAAATACAGAAATTACATTGATAACTGCAGTGGTATAATGCAAATATACT
 ATTGTTACATGTGAAAAATTGACTTAAAGTTATTGTTAAAGTATTGTTGGCTCCT
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 GCCTGCCAACGCTAGTGGAGAAGTCACCCCTGAGACCAGGTGTTAATCAAGCAAGCTGTAT
 ATCAAAATTGGCAGAAAACACAAATATGTCATATCTTTTAAAGTATTCA
 TTGAAGCAAGCAAATGAAAGCATTTACTGATTGTTAAAATTGGTGTGTTAGATATATT
 GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACCTCCAGCACCTAATGGAACCACATT
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 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRGRAQPPLLPLSLLALLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPPDTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSLKRLDLTNNRIGCLNADIFRGLTNVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPELPSFYMTP
 SHRQVVFEGDSLPFQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCISLIASALT
 ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRPRTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPLNL
 TNAVATARQLLAYTVEAANFSKMDVIFVAEMIEKFGRFTKEEKSKELGDVMDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596**N-myristoylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

GC GT GGGG **ATG**TCTAGGAGCTCGAAGGTGGT GCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATT CGGAAAAAGAAAACATT CGTCTTTGGGAGAACAGATTA
TTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAA
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTGTGTGTGTTGAT
GGAGAGTAGCTTAGTATCTTCATCTTTGGTCACTGTCCTTTAAACTTGATCA
AATAAAGGACAGTGGGT CATATAAGTTACTGCTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTACTGAGAACGACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAAC
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVVLGLSVLLTAATVAGVHVQQWQQQLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGQSQKS

Signal peptide:

amino acids 1-21

FIGURE 19

CTGTCGTCTTGCCTAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTT
 CAAGTGTGGCTTAATCCGTCTCCACCACCAAGATCTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCGCACCACCATACAACCACACGACGTATCTCGGG
 CCTGGGGTCCCCATGATCGTGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTCGC
 CTGCTGCAGCTGGTGTCTACCTGCCTGGCCTCTCGCTGGTGGCTAGCGTGGCGCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTCTGCTTCTCCGTGACCCCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTCCCCGTCTGGCGCAACTCCCC
 ATCACCTTCGCCTGCTATGCGCCCTCTGCCTCTGCCCTCCATCATCTACCCCCACAC
 CTATGTCCAGTCCTGTCCCACGCCGTTCGCGGGACCACGCCATGCCGCCACCTTCTCT
 CCTGCATCGCGTGTGGCTTACGCCACCGAACGTGGCCTGGACCCGGCCGGCCGGCGAG
 ATCACTGGCTATATGCCACCGTACCGGGCTGCTGAAGGTGCTGGAGACCTCGTTGCCTG
 CATCATCTTCGCCTCATCAGCACCCAAACCTGTACAGGCCATCGCCATCCTGCTGAACCTGGG
 GCGTGGCGGTGTACGCCATCTGCTCATCCTAGCGGCCATGCCATCCTGCTGAACCTGGG
 GAGTGCACCAACGTGCTACCCATCCCCCTCCCCAGCTTCCTGTCGGGCTGCCCTGCTGTC
 TGTCCCTCTATGCCACCGCCCTGTTCTGCCCCCTCTACCAAGTCATGAGAAGTATG
 GCGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTG
 GCCTGGGACCGCCGACTGGCTGTGCCATCCTGACGCCATCACCTACTGGGTATGTGGC
 TGACCTGGTGCACTCTGCCACCTGGTTTGCAAGGTCTAAACTCTCCAAGAGGCTCC
 CGTTCCCTCTCAAACCTCTTGTCTTCTGCCAGTTCTTATGGAGTACTTCTTCC
 TCCGCCTTCCTCTGTTCTCTTCTGTCTCCCTCCACCTTTCTTCC
 CAATTCCCTGCACTCTAACAGTTCTGGATGCATCTTCTTCCCTTCTTGCTGT
 TTCCCTCTGTGTTGTTGCCACATCCTGTTCAACCCCTGAGCTGTTCTTT
 CTTTCTTCTTTTTTTTTTAAGACGGATTCTCACTCTGTCGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCCTGGTTCAAGCGATTCTCCTCC
 CCCAGCCTCCAAAGTAGCTGGGAGGACAGGGTGTGAGCTGCCGCACCCAGCCTGTTCTT
 TTCCACTCTCTTCTCATCTTCTGGGTTGCCCTGTCGGCTTCTTATCTGCTGT
 TTTGCAAGCACCTCTCCTGTCCTGGAGCCCTGAGACTTCTCTCCTGCC
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTGCAGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTCCTAGTCAGTGTGAC
 GTGTGTGTGTGTTGGGGGTGGGGTAGCTGGGATTGGCCCTCTTCT
 CCCAGTGGAGGAAGGTGTCAGTGTACTTCCCTTAAATTAAAAACATATATATATAT
 ATTGGAGGTAGTAATTCCAATGGCGGGAGGCATTAAGCACCGACCCCTGGGCTTAGG
 CCCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAATTGGCCAGGCTTACAGAACAC
 CCACTGCCCTAGAGGCCATCTTAAAGGAAGCAGGGCTGGATGCCCTTACCCAACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTSSSGLSPMIVGSPRALTQPLGLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLTFVACI
IFAFISDPNLYQHQPALEWCVAVYAICFILAIAILLNLGETNVLPPIPFPSSLGALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

GAACGTGCCACCAGCCAGCTAATTTGATTTTAGTAGAGACGGGGTTTCAACATGTTGGCCAGGCTGGTC
 TTGAACCGTGCACCATGATCCGCTCACCTCGGCCCTCCAAAGTGCTGGGATTACAGGCATGAGCCACTGACGC
 CTGGCCAGCCTATGCATTTTAAGAAATTATTCTGATTAGGTGCTGTGCTAAACATGGGCACACTACAGTGACCA
 AAACAGACTGAATCCCCAAGAGCCAAGGACAGTGGAGGAGACCAACAAGAAAAGAGACCA
 TTATTACTCACTATGACTAAGGGTCACAAATGGGTACGGTGTGAGAGTGATTTGTTAAGAGACTACAGAGGG
 AGGACAGACTACCAAGAGGGGGCCAGGAAAGCTCTGTGACGGGTGGTATTCAGCCAAACTGGAAGAATGA
 GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGGAGCACTACACTACACTTGGCCTGAGAA
 AATAGCATGGGATTGGAGGAGGCTGGGAAACACCAACTTCTGGCAGCTGGCAGGGCATTGAGGGCTTGAGA
 AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGGCAGGGACTTGCAGGTGGAATCATAGGTCTTATC
 AACAGATATGGGCAAGCAAAGCCAGGGAGAATTGATGTTAATGCTGAGGTTGGAGCCAGGCTAGATGGGACAG
 TGGTGGGTGATGCAAAGGAAAGAGGTCAGGAAGCAGGGCCAGACGTGGGAGAAGGTGTGGGGTTGGTTCCA
 TCTTGCAGTCTGCGGAATGTGGATGGAAGACCAAGAGGAGGAGCAAGGGCAGAGGGAAAGGGATCTTAA
 AGAAGTCTGGATGCCACACTCTCTTCTTCCCTCTCCCTCTCAGAGGTCTCACTCGTGGTTCTTCAT
 TTCCTGCCCTGCCTCCATCTCTGTGGGTGCTGGGAAAGTGGAGGATTAGCTGAAGTTTGCTTCTCGGGGCTG
 TCTGAATCTCATTGTTCTGGGAGGACATAATTACCTGTCTAGCTTCTTATCATCTTACATTCCCTGTAG
 CCACTGGGACATATGTGGTGTCTCTCTAGCTCTGTCTCCCTCATGCCCTTGCTGGTATGGCATGTTAG
 GGGGAAGGTCAATTGCTGTGAGGGGCACTGACTTTCAATGGTGTACCAAGGTGAATGTTGAGACACAGTC
 GCGATGCTGCCAACGTCGGCGAGGCCCTAACTATCAGGAGATCGCTGCGCTGGCAGGTCTCCCTGCATGGT
 ATGCAGCCCTCCCATGTTCGGCACTTGTCTTCTCTCCCTGTCAGGTGAATCTCAGCCCTTCTGGAACTGTTCT
 GTGAGTACATGCTGGGTCTCCCTTTCTCTCTGTCAGGTGAATCTCAGCCCTTCTCCACCCAAAGGTT
 ACATGGATCTAACTACTGCCACCCCTCCACCTCCCTGCACCTGTGCTCCCTGGCCTGGCTTACCAAGGCTTC
 TCCACCCCTCCCTATCTCAGGTATTCCAGGTGGTGAAGGACACGTGACCAAGCCTACCGCCATGGCCAGG
 GCGAGTGGCTCACCTATTGAGTGGAAAGGGCTGGAGCAAGCCAGTGACTCACCTGTCGCCCTGGAATCAGCCT
 TTCCCTCTATTAGCAGACCTCAGCGAGGGCAACAAGAGGTCGCTTGCAAGCAGGAGTGGCTGAGCAGTTGCCA
 TCGCGGAAGCCAAGCTCCGAGCATGGTCTCGGTGATGGCGAGGACTCCACTGATGACTCCTATGATGAGGACT
 TTGCTGGGGAATGGACACAGACATGGCTGGCAGCTGCCCTGGGCGCACCTCCAGGACCTGTTCACCGGCC
 ACCGGTTCTCCGGCTGTGCCAGGGCTCCGTGGAGGCCTGAGAGCGACTGCTCACAGACCGTGTCCCAGACA
 CCCTGTCCTAGTCTGTGCAAGCCTGGAGGATGGGTGTTGGCTCCCCGGCGCTGGCTCCAGCTGCTGG
 GCGATGAGCTGCTCTGCCAAACTGCCCCAGCCGGAAAGTGCCTCCGAGCCTGGCCACTGGAGGCC
 AGGACTCACTCTAAACTGCCCTCACAGAGTCTGCTTCCCCCGGGAGGAGGCCAGCCCCCTGCAAGG
 ACTGCCAGCCACTCTGCCAACACTAACAGGGCAGTGGAACGGCAGCGGAAGCCTCTGACCTGGCTCT
 GGGTGGTCTCTTAGATGAGGATGAGGCAGAGCCAGAGGAACAGTTGACCCACATCATGCCCTGGCAGTGGCATGCA
 TCCCCGGCTGCTGCCAGGGGAGGCCCTGTGCCCCAAGTGTGGGCTCAAGGCTCCAGCAGAGCTCCACAGCC
 TAGAGGGCTCCTGGAGCGCTCGCTTCTCGCTGTGTGTTGATGAAAGTGTGGAGAGGAGGCCAGGGCTG
 GGCTGGGGCGCATGCTCTGCCCACTCCGGGCTTGCCGGGGTTGCCCGGGGCTCTGGGATGGCTACA
 GCTGTGGCAGACAGTGATGTTCATGTTCTTAAATGCCACACACATTTCTCTGGATAATGTGAACCAACTA
 AGGGGGTGTGACTGGCTGTGAGGGTGGGGTGGGAGGGGCCAGCAACCCCCCACCTGGAGGGCTGG
 TCTCTCTGCTTTCTCTCACTCCGAGTCCATGTGCACTGCTGATAGAATCACCCCCACCTGGAGGGCTGG
 CTCCCTGCCCTCCGGAGCCTATGGGTGAGCCGTCCCTCAAGGGCCCTGCCAGCTGGCTCGTGTGCTTC
 ATTACACCTCTCCATGTCTCTAAATCTCTCTTTCTAAAGACAGAAGGTTTTGGTCTGTTTCACT
 GGATCTCTCTCTGGAGGCTTGGAAATGATGAAAGCATGTACCTCACCCCTTCTGGCCCCCTAATGG
 GGCCTGGGCCCTTCCAAACCCCTCCTAGGATGTGCGGGCAGTGTGCTGGCCCTCACAGCCAGCCGGCTGCC
 ATTACCGAGAGCTCTGTGAGGGAGGTGGAAGAAAGGATGGCTCTGGTGTGCCACAGAGCTGGGACTTCATGTT
 CTTCTAGAGAGGGCACAAGAGGGCCACAGGGTGGCGGGAGTTGTCAGCTGATGCCGTGAGAGGAGGAAT
 TGTGCCAGTGAGTACAGTCAGGGAGTGTCTCTTGTGAGGAAAGAAGGTAGAGCCTTCTGCTGAAT
 GAAAGGCCAAGGCTACAGTACAGGGCCCCCAGCCAGGGTGTAAATGCCACGTAGTGGAGGCCCTGGCAG
 ATCCCTGCATTCCAAGGTCACTGGACTGTACGTTTATGGTTGGGAAGGGTGGCTTAAAGAATTAAGGC
 CTTGTAGGCTTGGCAGGTAAGAGGGCCCAAGGTAAAGAACGAGAGCCAACGGGACAAGCATTCTATATAAGT
 GGCTCATTAGGTGTTATTTGTTCTATTAAAGAATTGTTTATTAAATTAAATATAAAATCTTGTAAATCTC
 TAAAAA

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPESHPKVHMDPNYCHPSTSLHLCS
LAWSFTRLLHPPLSPGISQVVKDHTKPTAMAQGRVAHLIEWKGWSKPSDSPALESAFSSY
SDLSEGEQEAEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

1000 1500 2000 2500 3000 3500 4000 4500 5000 5500 6000 6500 7000 7500 8000 8500 9000 9500

GGTCCTGGCGCTCTGTTACACAAGCAAGATAACGCCAGCCCCACCTAATTTGTTCCCT
 GGCACCCCTCCTGCTCAGTGCACATTGTACACTTAACCCATCTGTTTCTCTAAATGCACGA
 CAGATTCCTTCAGACAGGACAACGTGATATTCAGTCAGTTCTCATCTGCAAAATGGCATAA
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTCAGTTCTCATCTGCAAAATGGCATAA
 TACAATCTATTCTGCCACATCAAGGGATTGTTATCCTTAAAAAAAACCAATACCAAAG
 AAGCCTACAATGTTGGCCTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTTT
 TTAAAACAATGAAAATAACCTATTCTTGAAAGTGAAGCAAACCTAAACTCAGATAAA
 GAAAATATAACCACCTCAAATCTAAGGCGAGTCATTCCCCTCTTGAATCTACCCAACAA
 CAGCCACGGAATAACAGATTCTCCAGTAACTCATCAGCAGAGCATTCTTGGCAGTCTAA
 AACCCACATCTACCATTCCACAAGCCCTCCCTGATCCATAGCTTGTCTAAAGTGCCT
 TGGAATGCACCTATAGCAGATGAAGATCTTGGCCATCTCAGCACATCCAAATGCTACACC
 TGCTCTGTCTTCAGAAAACCTCAGTTGGCTTTGGTCAATGACACCGTGAAAACCTCTGATA
 ACAGTTCCATTACAGTTAGCATCCTCTCTCAGAACCAACTCTCCATCTGTGACCCCCCTG
 ATAGTGGAACCAAGTGGATGGCTTACACAAAACAGTGATAGCTTCACTGGTTACCCCTTA
 TCAAGAAAAAAACAACCTCTACAGCCTACCTAAAATTCAACCAATAATTCAAACACTCTTCAA
 ATACGTCAAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTGGGGCCATTTAGGT
 GCTATTCTGGGTGTCTATTGCTACTCTTGTGGCTACTTGTGTGGAAAAGGAAAAC
 GGATTCAATTCCCCTGGCGACTTTATGACGACAGAAATGAACCAAGTTCTGCGATTAGACA
 ATGCACCGGAACCTTATGATGTGAGTTGGATTCTAGCTACTACAATCCAACCTTGAAT
 GATTCAAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
 TCCACTTCGTACTCTGTATAGAACTAACAGCAAAAGGCGTTAACAGCAAGTGTCACTA
 CATCCTAGCCTTTGACAAATTCACTTTCAAAAGGTACACAAAATTACTGTCACTGGAT
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACCGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTCTTACAATTGGCCATCCTGAGGCATTACTAAGTAGCCTTAATT
 TGTATTAGTAGTATTCTTAGTAAAGGAAATTGTGGAATCAGATAAAACTAAAGATT
 TCACCAATTACAGCCCTGCCTCATAACTAAATAATAAAATTATTCCACCAAAACTCTAAA
 ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCAATAATTCAAGATTGCAT
 TTTCTTAAATGAAAATTGAAAGGGCTTTAAAGAAAATTGACTTAAAGCTAAAAGAG
 GACATAGCCCAGAGTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
 TAGTACGTTATAATTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGCCATGGCAGGAAAGCTGACCCCTACCCAGGAAAGTAATAGCT
 TCTTTAAAGTCTCAAAGGTTGGAAATTAACTTGTCTTAATATATCTTAGGCTTCAA
 TTATTGGGTGCCTTAAAACCAATGAGAATCATGGT

FIGURE 24

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTSNDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNDSA
MPEEENARDGIPMDDIPPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTACCGCGC
 AGCCCGAAGATTCACTATGGTGAAAATCGCCTTCAATAACCCCTACCGCCGTGCAAAAGGAGG
 AGGCAGCGCAAGACGTGGAGGCCCTCCTGAGCCGACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTCATTCATCTGGCAGGACTTATTGTTGGAGCCTGCATTACAAGTACT
 TCATGCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTGATTCTGAGGATCCTGCA
 AATTCCCTCGTGGAGGAGGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCTGTGATAGTGACCCCTGCA
 CAATTATTGACTTTGAAAAGGAATGACTGCTTACCTGGACTTGGCTGGGAACACTGC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTGATGTTAGTAACCTGGCATCTTATTACCAACTTGCAATAACAGA
 AAGTCCTCCGCCTCGTCGCAGAGACCTCTGCTGGGTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTCCCCAACGAATTATTGTTGAGACCAAGATCTGTCAAGAGT
AAGAGGCAACAGATAGAGTGTCTGGTAATAAGAAGTCAGAGATTACAATATGACTTAA
 CATTAAGGTTATGGGATACTCAAGATATTACTCATGCATTACTCTATTGCTTATGCTT
 AAAAAAAGGAAAAAAAAAACTACTAACCAACTGCAAGCTCTGTCAAATTAGTTAAT
 TGGCATTGCTTGTGAAACTGAAATTACATGAGTTCATTTTCTTGCAATTAG
 GTTGTGTTTTGTGTTGTTGTTCTTCTTAAGTAAGCTTATTACATCTTATG
 GTGGAGCAATTAAAATTGAAATATTAAATTGTTGAACTTTGTGTAAAATATA
 TCAGATCTCAACATTGTTGGTTCTTGTGTTCTTGTACAACATTCTGTAAATTAGA
 AATTACATCTTGCAGTCTGTTAGGTGCTCTGTAATTAAACCTGACTTATATGTGAACAAATT
 TTCATGAGACAGTCATTAACTAATGCAGTGATTCTTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTTGTATGAATTCTACAA
 CCCTATAATAAATTACTCTATAACAAAAAA

FIGURE 26

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
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ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFIFYQLCNNRKSFRRLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCCAGCCCAGAGCAGCCCCGGCACAGCACGGACTCTCT
 CTTCCAGCCCAGGTGCCCCCCACTCTCGCTCCATTGGCGGGAGCACCCAGTCCTGTACGCC
 AAGGAACTGGTCTGGGGCACCATGTTCGGCAGCCCCAGCCTCCTCATCCTCTG
 TTGCTGCTGCTGGGTCTGTGCCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGAGGCCAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCCTGGACCCCAGGCCCTAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGG
 GGCCCACATCACCCCCCACCACCTCCTGGATGGGATAGTGGACTTCTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGCTCCCTGGCCTTCTGCTGATGTTCATCGTCTGTGCCCGGTCA
 TCACCCGGCAGAACAGCAGAACAGGCCTCGGCCTATTACCCATCGCCTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCAGGAAGCCCTGGATTCCCTCCCGCAGCTCCAGGCCACATCTGGCCG
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCAGTGGCGGTGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAACGGCAGCCAGGAGGGGACCAGGAAGTCCA
 GGGACATGGGTCCCAGTGGAGACACCAGAGGCCAGGAGGAGCCGTGCTCAGGGTCCTTG
 AGGGGCTGTGGTGGCCGGTGAGGGCAAGGGAGCTGGAAGGGTCTCTTTAGCCAG
 GAAGCCCAGGGACCAGTGGTCCCCCGAAAGCCCTGTGCTGCAGCAGTGTCCACCCCCAG
 TGTCTAACAGTCCTCCGGCTGCCAGCCCTGACTGCTCCTGACACTCCCTCCTGGCCTCCCTGTGG
 GTGTATGAAAAGGCCTCAGCCCTGACTGCTCCTGACACTCCCTCCTGGCCTCCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTCCCCGGA
 GGAATCTTACCAAGTGCATCATCCTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGATTACAGGCGTGAGCCACCGTGCCGGCCCAAACACTTTTAAACAA
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTCTGAAGG
 TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCCGGCTGGGGTGAGTTCTCATCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTGAGGGGACCTCCACCCCTGGGAAGTCCGAGGGCTGGGAAGGGTTCTGACG
 CCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGCTGGCAGCCTG
 TGTCCACAATATCGTCAGTCCTCGACAGGGAGCCTGGCTCCGTCCTGCTTGGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACAATAAACCTTATTCCGGCCTGAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAPSLILLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSIAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVTQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLQAQEAQGPVGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGGAAGGAGGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAGATG
 AAGTTCCAGGGGCCCTGGCCTGCCTCCTGCTGGCCTCTGCCTGGCAGTGGGAGGCTGG
 CCCCCTGCAGAGCGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGCC
 TGGGAGACGCCCTGAGCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTGGCAAGGGACAGAGAAGCAGTGGCACTGGAGTCAG
 GCAGGTTCCAGGCTTGGCGCAGCAGATGCTTGGCAACAGGTGGGAAGCAGGCCATG
 CTCTGGAAACACTGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCA
 GATGCTGTCCGGCTCCTGGCAGGGGTGCCTGGCACAGTGGCTTGGAAACTTCTGG
 AGGCCATGGCATCTTGGCTCTCAAGGTGGCCTGGAGGCCAGGGCAATCCTGGAG
 GTCTGGGACTCCGTGGTCCACGGATACCCGGAAACTCAGCAGGCAGCTTGAATGAAT
 CCTCAGGGAGCTCCCTGGGTCAAGGAGGAATGGAGGCCACCAAACCTTGGACCAACAC
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTCAGTGAGAGGCCAGCAACCAGAATGAAGGGT
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGAGGCAGCGGC
 TCACAGTCGGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGTGGCAGCAGTGG
 TGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCAGCAGTGGCAGCAGTGG
 TCCAGCACCGGCTCCTCCGGCAACCACGGTGGAGCAGGGAGGAAATGGACATAAAC
 CGGGTGTAAAAGCCAGGGATGAAGCCGGAGCAGGGAAATCTGGGATTAGGGCTTCA
 GAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTTGG
 GGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGAGTGGAGGTGACGCTGT
 TGGTGGAGTCATACTGTGAACTCTGAGACGTCTGGATGTTAACCTTGACACTTCT
 GGAAGAATTAAATCCAAGCTGGTTCATCAACTGGATGCCATAAACAGGACCAAGAGA
 AGCTCTGCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGAGCCACACT
 CCCTCCTTAAACACCACCTCTCATCACTAATCTCAGCCCTGGCAGGAAATAACCTTA
 GCTGCCCAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPSGSGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSGGSSGSSGGSSGGSSGSGSNGSRGDSGSESSW
GSSTGSSSGNHHGGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
GGSGDNYRGQGSSWGSGGGDAVGGVNTVNSETSPGMNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGGTCCCTCCGGTCCCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGCGGTGCTCACCG
 TGCCTGGCTGGGGAGTTCTCTCCTTGCTGACCATGTTGTCCTGCTGGAATTACCGGGACATCTTCA
 CTCTCCTGCTGCCCTGCACCCGGAGCTTGGTGTGCGAGGAGACTGAGGGAAAG**ATG**TGTTTCTGAACAAGC
 TGCTGCTACTTGCTGCTGGCTGGCTTCCAGATTCCCAGTCCCTGAGGACTTGTTCTTCTGGAAGAGG
 GTCCCTCATATGCCCTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTGGACAATGCGCCCTGTTGGTGGACCAGC
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAAACTGCTCGCTCGTGGGTGTCAGGCAGTAGTG
 GACGGAGTGGGGCCTCATGAGGAAAATCACCCCCACCACTACCACACCAGCTGGGAGCCAGCCTTCCCAGACCA
 GCCAGGGGCTGCAGGCACAGCTGCCAGGCCTTTCCACAACCAGGCCCTCCTGCGCCGACCAGTAGAGT
 TCGTGGCAGAAAGAATTGGATCAAACATGTGTCACAGACTGAGGCTACACTGGTGGCAGATCTGGTGCAGCAGG
 CAGAGTCACCTCTCAAGAGCAGCTGGTACACAGGGAGAGGAAGGGGGAGACCCAGCCAGCTGTTGGAGATCT
 TGTGTTCCAGCTGTGCCCTACGGGGCCAGGCATTGGCCTGGGGGGAGTTCTGTCAGGAAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTCCAGAGGAGACCCGGCAGCGTTCTGAGCAGTGAGAGAACATTGCTGTGGGC
 TTGCAACAGAGAAAGCCTGTGCTGGCTGTAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTCGCACACTTCGAGCCCAGGTCTGAACCTGCTGCCGGGGGGAGCGGAGGGCTGCTCCGCGC**TGAC**
 GTGCTCTCTGGCCGTGGGGCACGGGACCTGACGAGGGAGTCTCCCAGAGCATTGAAACAGCTCTAGGC
 CAGCTGGCCAGACGCTGCGGTGCCAGTCTGCCCCACTGCTGAGCAGCATTGCAAAGTGCTCTGTG
 GAGTTAGCTCCCTCTCGTTGCAAGATAAAATTCTATCCTAGGGCCCCCGCACAGTACAGGCTGGAGAGAGGG
 CAGGCTCGAAGGCTCTGCACATGCTGCTTCTGAGGAAAGACTTCAAGGGCCGGTCTCGCTGAGCTG
 CTGCTGAGCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCAAGGGAGTGGACTTCTGCTGCTATTCTGCTA
 CGGGAGCTGGTGGAGAAGGGCTGTGATGGGACGGATGGAGATAAGAGGCTGCTGGCAGCCTCACCAGGCCAG
 TGGCCAGGGACTTTGCTGAAGAATTAGAACACTGCTAATCTGTTCTAGGCCAGGCCCCACCTGCCAGAACCC
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCAACAGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCTTGGGATTGACCAAGAACCCCTGACCCCCGGCTCACAGGAGGGCCAAGTGCCAATGCAAGACCCCTCAC
 TGGTTGGGTGTAAGCTGGCTACAGTCAGACTTCTGCTCTAAGGGTGTCACTGCCCTGGCATCCCACACCGA
 ATCCTACAGGAAGGAGAGTTGCCCTGATTGGATTATGGCAGAAAAGTCAGAGATGCCAGTCCTGGAGTAGAA
 GAGGTGGTGGTTGTTATCTCTGGATACTAAATGAAATGAGGTGTGTTGCTGCAACACAGAATTCAAGCCT
 CATTTGCTATCCCAGCATCTCTAAAACCTTGTAGCTTGGAAATTGACAGAGGCAAATGACTCCTGCTAAC
 TTATGAAGAAAGTAAACATGAATCTGGGAGTCTACATTCTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT
 ATAAATGCCTAACACAGGCCGGTCTGGGCTCATGCCCTGTAATCCAGCACTTGAGAGGCCCTGAGGTGGCG
 GACTGCCCTGAGGTCAAGGAAATTCAAGACCAGCCTGCCAACATGGAAAACCCATCTACTAAAAAATAAAAAA
 TTATTAGCTGGGATGGTGTGCTGCCCTGTAATCCCAGCTACTCAGGAGGATGAGGAGGACCTGCTTGAAC
 CTGGAGGTGGAGGTGCACTGAGCCAGGGTGCACCCACTGCACCTCAGTCTGGTAACAGAGCAGACTTCTAG
 AAAAGCCTAACAAACAGATAAGTAGGACTCAACCAACTGAAACCTGACTTCCCCCTGTACCTCAGGCCCTG
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTTAGAGCTTTAGAATAAA
 CTGGTTTCTTAAAAAAAAAAAAAAAGGGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTTTTAAAGGGCTTTATTAAATCTCCOCACAGTGGCTCTGCAATCTGCCACAGCTC
 TGGGGCGTCTGTAGGGAAAGGCCCTGTTCTGAGGCGGGCTGGCTTGTCCATGGGTCCGGAGCTG
 GCGCTGCTGGGCCCTGGCGTGTGCTAGCTGCTCTTGCCGGCACAGAGCTGCGGGCTGGGGCACCAGGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGGGAGGCGCTGTCTTAACCGACACCCCTGAGGTGCTCTGAGATGCTG
 GGTCCACCTGAGTGGCACGGGAGCAGCTGTCGGCTTCTCYAGGCCAGTCTGGGAAACTAAGCTC
 GGGCCCTCTTGCAAAGACCGAGGATGGGTGGGTGGGGACTCATGGGAATGCCCTGAGGAGCTACGTGT
 GAAGAGGGCGCCGGTTGTTGCTGCAGCGCCTGGAGCGCCTCTCTGAGCCTCAGTTCCCTTCGCTTA
 ATGAAGAACATGCCCTCGGTGCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTGGACGAGCGTCAT
 CTTATTTCACAACTGTCCTGCGACGTTGGCCTGGCACGTCATGGAATGCCCATGTCCTCTGCTGCGTGGAC
 GTCGCGGTGGAGTGGCAGGCCAGAGGCCAGGGCTCCCGCCGCCGCCACCACCGTCCAGG
 CCTCACAGGAAGTTGGCTCCCGCACCAAGGCAGGGCGGGCTCCCGCCGCCGCCACCACCGTCCAGG
 GGCGGTAGACAAAGTGGAAAGTCGCGCTTGGCTCGCTGCGCAGCAGGTAGCCCTGATGCACTGCCAGCGC
 TCGTCCGCCAGCTGGAAGCAGCGCCGTCACCAGCACGAACAGCCGGTGGCCT

FIGURE 32

MCFLNKLLLLAVLGWLFOIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTSLGAQPSQTSQLQAQLAQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLVALVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAASRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTCGGGGTCACTGAAGGCTGTCTGATCAGGAAACTG
AAGACTCTCTGCCACAGCAGTTCTGCAGCTCCTGAGGTGTGAACCCACATCCC
TGCCTCCAGGGCACCTGCAGGACGCCACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
AGTAGCAACAAAGAGCAGCGGTCAAGCAGTGGCATCAGTGGCTATGCCATTCTCGC
CATCCTCTACAGCTCAACAGTCCAATGAGGTCTTCATTACGGCTCCCTGCAGGGCGTA
GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCAGTGGCTATGCCATTCTCGC
AACAAAGACACTGCCCTCTCGGTGCCACCAGTGTGATTGTCAAGCAGCTCCAGCACCTGCT
GGGCACCAAGCTGGGCCCTGAGATCGAGCAGGGCTGAGTGTACAATCCGCATGAATGATGCAC
CCACCACGGCTACTCAGCTGATGTGGCAACAAGACCACCTACCGCGTGTGGCCATTCC
AGTGTGTTCCCGGTGCTGAGGAGGCCAGGAGTTGTCAACCGGACCCCTGAAACCGTGT
CATCTCTGGGGGCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCCTGATCC
AGCGAGCAGGGCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCCGGCCATGCGG
CAATTGACGACCTCTCCGGGTGAGACAGGGCAAGGACAGGGAGAAGTCTCATCGTGGTT
GAGCACAGGCTGGTTACCATGGTGATCGCGGTGGAGGTTGTGACCACTGCATGTCTATG
GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGCCCGCCTCAGCGCATGCCCTACCACTAC
TACGAGCCAAAGGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG
CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTCTCATCGTGGGCCAGCTGTATGGCA
TCACCTTCTCCCACCCCTCGGAC**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
AGGAGAACGAGCTCCGCCAGCCCTAGGCCAGGGACCATCTCTGGCAATCAAGGCTTG
CTGGAGTGTCTCCAGCCAATCAGGGCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
TGGGAATCTGTTGGCAATCAGGGATTGGGAGTCTATGTGTTAATCAGGGGTGTCTTC
TTGTGCAGTCAGGGTCTGCGCACAGTCAGGTAGAGGGGTATTCTGAGTCATCTG
AGGCTAAGGACATGTCTTCCATGAGGCCTTGTTAGAGCCCCAGGAATGGACCCCCCA
ATCACCTCCCCACTCTGCTGGATAATGGGGCCTGTCCTCAAGGAGCTGGAACTGGTGTG
CCCCCTCAATTCCAGCACCAGAAAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC
GGCCAGAGAACATTGTGGGGTTGGAGGTTGTGGGGGGCGGTGGGAGGTCCCAGAGGTGGGA
GGCTGGCATCCAGGTCTGGCTGCCCTGAGACCTGGACAAACCCCTCCCCCTCTGG
CACCCCTCTGCCACACCAGTTCCAGTGCAGGAGTCTGAGACCTTCCACCTCCCTACAA
GTGCCCTCGGGCTGTCCTCCCCCTGGACCCCTCCAGCCACTATCCCTGCTGGAGGCT
CAGCTCTTGGGGGTCTGGGTGACCTCCCCACCTCTGGAAAAACTTGGTATTTTG
GCAAACCTCTTCAGGGTGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTCT
TAGCCCTCAGCCAGCTGCCATTAGCTGGCTCTAAAGGGCAGGCCCTCTGGAGTCTGCC
CTAGCAGGGAGGTTTCCAACGTGGAGGCGCTTGGGCTGCCCTTGTCTGGAGTCA
CTGGGGCTCCGAGGGTCTCCCTGACCCCTGTCGTCCTGGATGGCTGTCAGGGAGCTGT
ATCACCTGGTTCTGCTCCCTGGCTCTGTATCAGGCACTTATTAAAGCTGGCCTCAGTGG
GGTGTGTTGTCCTCTGCTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGTGG
GGCGGGTGACTIONGCCAGACTTGGTTGTAATGATTGTACAGGAATAAACACACCTACGC
TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCVIVSSSSHLLGPKGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
SSVFRVLRRPQEfvNRTPETVFIWGPPSKMVKPQGSLSRVVIQRAGLVFPNMEAYAVSPGRM
RQFDLFRGETGKDREKSHSWLSTGWFTMVIATELCDHVHVVGMVPPNYCSQRPRLQRMPYH
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCTCATAGTGGCGTCTCTAAAGGAAAAAACACTAAAATGAGGAACCTAGCGGGACCGGAGCGACGCAGCTT
 GAGGGAAAGCATCCCTAGCTGGCGAGAGGGCGAGGCTGAAGCCGAGTGGCCGAGGTGTCGAGGGGCTGG
 GCAAAGGTGAAAGAGTTCAAGAACAGCTCCTGAAACCCATGACCCATGAAGTCTGTCGACATTATACCGT
 CTGAGGGTAGCAGCTGAAACTAGAAGAAGTGGAGTGTGACACCACTGGCTTGACCCAGGGACGGCAGTATCTCTTGTGACCCCTGGC
 GGCCTATGGGACGTTGGCTTCAGACCTTGTGATACACC**ATG**CTGCGTGGGACGATGACGGCGTGGAGAGGAATG
 AGGCCTGAGGTCAACTGGCTTGCCTCCCTAGCACAGCAGGCTGCTTGACTTGAACGAGGTCCCTCAG
 GTCACCGTCCAGCCTGCGTCCACCGTCCAAGGCCGGAGGACTGTGATCTTGGGCTGCGTGGGAACCTCCA
 AGGATGAATGTAACCTGGCGGCTGAATGAAAGGAGCTGAATGGCTGGAGTGTGATGTCCTGCTCATCACC
 CACGGGACCCCTGTCATCATGCCCCCTAACACAACCAACTGTGGGACGGTACCGTGTGGCCGGATGCGCTGCG
 GGGGCTGTCAGCGTGCAGCCACTGTGACACTAGCCAATCTCAGGACTTCAAGTTAGATGTGACGACGTG
 ATTGAAGTGGATGAGGGAAACACAGCAGTCATTGCTGCCACCTGCTGAGAGGCCACCCCAAAGCCCAGGTC
 TACAGCGTCAAACAAGAGTGGCTGGAGGCTCAGAGGTAACCTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGGCATGTACAAGTGTGACGCCCTAACACCCAGTGACCCAGGAAGTGA
 ACCCTGGCTCCAGCGCAGGCTACGTGTGCGCCCTCACCGCTGAGGCTGCCGCATCATCTACCCCCCAGAGGCC
 CAAACCATCATGTCACCAAAGGCCAGAGTCTCATCTGGAGTGTGCGGCTAGGAAATCCCACCCCCACGGGTC
 ACCTGGGCCAAGGATGGGTCCAGTGTGACCGGCTACAAACAAGACGCGCTTCTGTGAGGACAACTCCTCATCGAC
 ACCACCAAGCGAGGAGGACTCAGGCACCTACCGCTGATGGCCGACAATGGGTTGGGCGAGCCGGGAGCGGTC
 ATCCTCTACAATGTCCAGGTGTTGAACCCCTGAGGTACCAGGAGCTATCCCAGTGGTCATCCCCCTGGG
 CAGAGTGCAGCTTACCTGTGAGGTGCGTGGGAAACCCCCCGCCCTCGTGTGGCTGAGGAATGCTGTGCC
 CTCATCTCCAGCCAGGCCCTCGGCTCTCCCGCAGGGCCCTGCGCGTGCAGCATGGGCCTGAGGACGAAGGC
 GTCTACCAAGTGCATGGCGAGAACAGGGTTGGGAGGCGCCATGCGCTAGTCCAGTGGCGGACCTCCAGGCCAAGC
 ATAACCCAAGGCTATGGCAGGATGCTGAGCTGCTACTGGCACACCTCTGTATCACCTCCAAACTCGGCAAC
 CCTGAGCAGATGCTGAGGGGCAACCGGGCTCCCCAGACCCCCAACGTCAGTGGGCTGCTTCCCCGAAGTGT
 CCAGGAGAGAAGGGGAGGGGCTCCCGCAGGCTCCCATCATCTCAGCTCGCCCCGACCTCCAAGACAGAC
 TCATATGAACTGGTGTGGCGGCCCTGGCATGAGGGCAGTGGCCGGCGCAATCCTCTACTATGTGGTGA
 CGCAAGCAGGTCACAAATTCCCTGACGATTGGACCATCTCTGGCATTCCAGCCAACCAGCACGCC
 ACCAGACTTGGACCCCCGGAGCTGTATGAAGTGGAGATGGCAGCTACAACTGTGCGGGAGAGGCCAGACAGC
 ATGGTCACCTTCCGAACTGGACGGCGCCAAACCCGAGATCATGGCAGAACAGAGCAGCAGATCCAGAGAGAC
 GACCCGGAGCCAGTCCCCAGAGCAGCCAGCCAGACACCGCCCTCTCCCCCCCCAGAAGCTCCGACAGG
 CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGATGGTGGTTCC
 CAGTCCTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGAGACTGGATTCTGGCACCAGGCC
 ACCAGACTTGGGGAGGATACGGGACACTGGCACTCCATCAGGCCACCTGAGGCCAGAGACCTCC
 GACATTAAGATGCACTGCTTCATGAAGGAGGGAGAGCGAGTCAGCAACGTGATGTCGTGAGACCAAAGCT
 CGGAAGTCTCTGGCCAGCCTGGTCACTGCCACCCCAACTCTGGCCACCCACAGCCGCCCTCTGAA
 ATAGAGCGGGCGGTGGCACTGGGCCATGGTGGCTCGCTCCAGCAGCCTGCCCTATCTGATTGTGGGGCTGTC
 CTGGGCTCATCGTCTCATCGTACCTTCATCCCCCTCTGCTGTGGAGGGCTGGTCAAGCA
 ACAACAGACCTGGGTTTCTCGAAGTGCCCTTCCACCTCTGTGATA
 ACTATGGTGCCTTGGGAGGACT
 CCAGGCCACCGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
 AATAGGGCTGCCCTCGGCTGAGTGGCTACCCGGGAGTGAAGCCCCAGCAGCACTGCCAGGGAGCTTCAG
 CAGCAGAGTACACAGCAGCAGCTGAGGAGACGACCTTGGCAATGGATATGACCCCAAAGTCACCA
 AGCAGGGGCTCCAAGTCTAGCCGGAGGGCTTCTTCTTACACACTGCCGAGCCTCCACTCAGCAGCTG
 CTGCAGCCCCATCAGCACTGCTGCAACGCCAGGAGCAGCCTGCTGTGGGGCAGTGGTGCCTGG
 CCCGACAGTCTGCTGGAGCAGTGTGGGACCCCTCATTTCACTCAGGGCCCCCATGCTGCTGGGCTTGTG
 CCAGTTGAAGAGGGTGGACAGTCTGACTCTGCCAAGTGTGAGTGGAGGAGACTGGTGTCCCAGC
 ACCTGGGCTTGGGAGGAGGACT
 GCCTACGTAGGACAGGAACCTGGAATGCACTCTCCCCGGGGCACTGGTGC
 GTGTGCTTTGAAACACCA
 CTCACAAATT**TAGG**CAGAAGCTGATATCCCAGAAAGACTATATATTGTTTTTAAAAAAAAGAAGAAAA
 AGAGACAGAGAAAATTGGTATTATTTCTAATTAGCCATATTATATATTGTA
 ATGTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTTGGAGGGAAAATAAGAAGCTGCCA
 CCTAACAGGAGTACCCAGGAAAGCACCGCACAGGCTGGCGGGACAGACTCCTAACCTGGGCTCTGCA
 GCAGGGAGGCTGCAGGAGGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTC
 CATCACGAGCA
 TGAGGGACAGCAAGGGGACGGTATCACAGCCTGGAGACACCCACACAGATGGTGGATCCGGTGC
 ACAGGGAA
 ACATTTCTAAGATGCCATGAGAACAGACCAAGATGTGACAGCACTATGAGCATTAAAAACCTCC
 AGAAT
 CAATAATCCGTGGCAACATATCTGTAAAAACAAACACTGTA
 ACTTCTAAATAATGTTAGTCTTCCCTGTAAAA

FIGURE 36

Protein sequence

MLRGTMATAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVLGCVVEPP
 RMNVTVRLNGKELNGSDDALGVILITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSTGSSDRLVRVRSTAAARIIYPPEAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQLRLS
 RRALRVLSMGPEDEGVYQCMAENEVGSAAHVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSGPASPCKCPGEKGQGAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTRGRRPKPEIMASKEQQIQRDDPGASPQSSSQPDHGRSPPEAPDRPTISTASE
 TSVYVTWI PRGNNGGFPIQSFRVEYKKLKVGDWILATS AIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPS RPYVVSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNT
 PIHGFYI YYRPTDSDNDSDYKKDMVEGDKYWH SISHLQPETSYDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
 IIIVTFIFCCLWRAWSKQKHTTDLGFP RSALPPSCP YTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRCPSA AVG YPGM K PQQHCP GE LQQQSDTSS LLRQ THLG NGYDPQ SHQ IT RGPK
 SSPDEGSFLYTL PDDSTH QLLQPHHDCCQRQE QPAAVGQSGV RAPD SPV LEAVWD PPFHSG
 PPCC LGL VPVEEV DSDC QVSGGD WCPQHPVGAYVGQ EPGM QLSPGP LVRV SFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTGTCATGATCCGGACCCATTGTCGGCCTCTGCCCATGCCCTGCTCCTC
 CCAGGCTCCC CGGGCCACCCCCCGCGAACATGCAGCCCACGGGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCCAGC
 CCGTAACCCCGCGGGAGACCACGCCGGCGCCCCAGAGCCCTCTCCACGCTGGCTCCCC
 AGCCTCTTACCAACGCCGGGTGTCAGGCCCTCACTACCCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCCCTGGACCTTCGGGTCGCGCGAGGCCCTGATGCGGAGTTCCCACCTG
 TGGACGGCCACAATGACCTGCCAGGTCTGAGACAGCGTTACAAGAAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCCTACTCTGAACACTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTAAAAGCTGCCCTGCCTCATTGGCGTNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCCAGTTCTATGTGCTGGGGTGCGCT
 ACCTGACACTTACCTCACCTGCAGTACACCAGGGCAGAGAGTTCCACCAAGTTCAGACAC
 CACATGTACACCAACGT CAGCGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGGAGTTGAA
 CCGCCTGGCATGATGATAGATTGTCCTATGCATGGACACCTTGATAAGAAGGGTCTGG
 AAGTGTCTCAGGCTCCTGTGATCTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTG
 TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGTGCTGCAGTGCAACCTGCTGCTAACGTGTCCACTGTGGCAGATCACTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATGGGATTGGGAAATTATGACGGGACT
 GGCGGGTTCCCTCAGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTCGTGGAAACCTGCTGCC
 TCAGACAAGTGGAAAAGGTGAGAGAGGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT
 CCATATGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATGGGCTCCCTGGAGGTCTCAAATGCCT
 CCCCATACTTGTCCAGGCCTGTGGCTGCCACCATCCAAACCTCACCCAGTGGCTC
 TGCTTGACACAGTCGGTCCCCGCAGAGGTACTGTGGCAAAGCCTCACAAAGCCCCCTCCT
 AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pi: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWASVSCSQDQTAVRLALEQIDLIHRCASYSSELELVTSAEGLNSS
QKLAACLIGVXGGHSLDSSLVLSFYVLGVRYLTLFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRLEVSQAPVIFSHSAARAVCDNLLNPDDILQL
LKNGGIVMVTLMSGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVILIEELLSRXWSEEELQGVLRGNLLRVFRQVEKvreesRAQS PVEAEFPYQQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTGCTGCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTGGTGGCTGTGGTCGGGTGTTGCTGGTGCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTACATTGTACATCACCTGTCCGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCCCTGTATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCTCGATGGCACAAAGATGCTCAGC**TAG**ATGGGCTGG
 TGTGGTTGGGTCAAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTCCCTCGGTTCCAGTCTCCCTTAAAAGCCTGTGGCATTTCCTCCTT
 CTCCCTAACCTTAGAAATGTTGACTTGGCTATTTGATTAGGGAAAGAGGGATGTGGTCTCT
 GATCTCTGTTCTTGGGTCTTGGGTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTGAGGCCCTCAGGAGTGGATGCGATCTGCTCTCCGGCTCCACTTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTGGAAAGATAAAAGCTGGGTCTTCA
 GGAACTCAGTGTCTGGAGGAAAGCATGCCAGCATTGAGCATGTGTTCTTGCAGTG
 GTTCTTATCACCAACCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCTGAGCCCACTGGGTCTTCAGGGTGCAGTGG
 AGCTGGTGGTCTGACTTCCCTGTGCACTTCTCGCACTGGGCATGGAGTGCCTGCATACT
 CTGCTGCCGGTCCCTCACCTGCACTTGAGGGTCTGGCAGTCCCTCCTCCCCAGTGTG
 CACAGTCACTGAGCCAGACGGTCGGTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCCGTACTTGGGTTGCCTTTGTCCTGAACCTCGTTGTAACAGTGCATGG
 GAGAAAATTTGTCCTTTGCTTAGAGTTGTGTAAATCAAGGAAGCCATCATTAAATTG
 TTTTATTCCTCTCA

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHDVEAYCLLCECRYEERSTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCAGGGTCTCGTTGGGTCGCTAATTCGT CCTGAGGCCTGAGACTGAGTTCATAGGGTCTGGGCCCCGA
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGCACCCAAAGTGAGGGGCCGTGTTGGGCTCTCCC
 TCCCTTGCAATTCCCACCCCTCCGGCTTGCCTTCTGGGACCCCTCGCCGGAGA**ATG**CCCGCTTGATG
 CGGAGCAAGGATTGCTGCTGCCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGAGT
 TCGCGGCCAAACTCAACTCCATCAAGTCTCTGGCGGGAGACGCCGGTCAAGCCGCAATCGATCTGCG
 GGCATGTACCAAGGACTGGCATTGGCGCAGTAAGAAGGGCAAAAACCTGGGCAGGCCTACCCCTGTAGCAGT
 GATAAGGAGTGTGAAGTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATGGCCTGATGGTGTGCGAGA
 AAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT
 ACTGAAAGCATCTAACCCCTCACATCCCGCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTATTAC
 TCAAACCATGACTTGGGATGGCAGAACATCTAGGAAGACCACACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTGCTGTGCTCGTCAATTCTGGACAAAATCTGCAA
 CCAGTGCCTCATCAGGGGAAGTCTGTACCAAACAACGCAAGAAGGGTCTCATGGCTGAAATTTCAGCGT
 TGCAGACTGTGCGAAGGGCCTGCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
 TGTCAAAAATT**TCA**TCACTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTATTAAATGCATTATAG
 CATGGTGGAAAATAAGGTTAGATGCAGAAGAACATGGCTAAAATAAGAAACGTGATAAGAATATAAGATGATCACA
 AAAGGGAGAAAAGAACATGAACTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
 CAACTTGTCTATGTAATAATGTACACATTGIGAAAATGCTATTATAAGAGAACAGCACACAGTGGAAATT
 ACTGATGAGTAGCATGTGACTTCCAAGAGTTAGGTTGCTGGAGGAGGTTCTTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTCTATTCAACGTTAGAGTTAACAAAATACTCCTAGAATAACTTGTAA
 TACAATAGGTTCTAAAATAAAATTGCTAAACAAGAAATGAAAACATGGGAGTGTAAATTACAACAGAAAAT
 TACCTTTGATTTGAAACACTACTTCTGCTGTTCAATCAAGAGCTTGGTAGATAAGAAAAAAATCAGTCAATAT
 TTCCAATAATTGCAAAATAATGCCAGTTGTTAGGAAGGCCCTTAGGAAGACAAATAAACAAACAAACAG
 CCACAAATACTTTTTCTAAAATTAGTTTACCTGTAATTAAAGAACTGATACAAGAACAAACAGTCC
 TTCAGATTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTGCTGATGCATTATATTTC
 AACTATACCCATAAAATTGTGACTAGTAAAATACCTACACAGAGCAGAATTTCACAGATGGCAAAAAAATTAA
 GATGTCCAATATATGTGGGAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCATAACCTATATT
 GATAGAATTAGATTGGTAAATACATGTATTCAACATACTCTGTTGTAATAGAGACTTAAGCTGGATCTGTACTG
 CACTGGAGTAAGCAAGAAAATGGAAAACCTTTCTGTTGTCAGGTTGGCAACACATAGATCATATGTCTG
 AGGCACAAGTTGGCTGTTCATTTGAAACCAGGGATGCACAGTCTAAATGAATATGCATGGGATTGCTAT
 CATAATTTACTATGCAGATGAATTCACTGTTGAGGTCTGTGCTCGTACTATCCTCAAATTATTATTTATAG
 TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTACAAAATGTAACCTCTGTAAGTAGACAGAGTAGTGAGG
 TTTCATTGCCCTCTATAAGCTCTGACTAGCCAATGGCATCTCCAATTCTCCCAAACCTCTGCAGCATCTG
 CTTTATTGCCAAAGGGCTAGTTGGTTCTGCACGATTGCCGTTAAAAAATATAAGTAGGATAACTTGTAAA
 ACCTGCATATTGCTAATCTATAGACACCAAGTTCTAAATTCTGAAACACTTTACTCTTTAAACTT
 AACTCAGTTCTAAATACCTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTGTGACTTTAAACTTTG
 TAGACCACAATTCACTTTAGTTCTTACTTAATCCCATCTGCACTCAAAATTAAAGTTCTCCCAGTAG
 AGATTGAGTTGAGCTGTATATCTATTAAAAATTCAACTTCCCACATATATTACTAAGATGATTAAGACTTA
 CATTCTGCACAGGTCTGCAAAACAAAATTATAAAACTAGTCCATCCAAGAACCAAAGTTGTATAAACAGGT
 TGCTATAAGCTTGAAATGAAAATGGACATTCAATCAAACATTCTATATAACAATTATTATTTACAAT
 TTGGTTCTGCAATATTCTTATGTCCACCCCTTTAAAATTATTATTTGAAGTAATTATTTACAGGAATG
 TTAATGAGATGTATTCTTATAGAGATATTCTTACAGAAAGCTTGTAGCAGAATATATTGCACTATTGAC
 TTGTAATTAGGAAAATGTATAAGATAAAATCTATTAAATTCTCCTCTAAAACGTGAAAAAA

FIGURE 42

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLSNIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKKRCHRDGMCCPSTRCNN
GICIPVTEILTPIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGT GATCCGCCTGACCTTGT AATCCACCTACCTGGCCTCCAAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCGGCCAACATCACGTTTTAAAAATTGATT
 TCTTCAAATT CATGGCAAATATTCCCTCCCTTAACTCTTATGT CAGAATGAGGAAGGA
 TAGCTGCATTATTTAGTCAGTTTCATTGCATAGTAATATTTCATGTAGTATTTCTAAG
 TTATATTTAGTAATT CATATGTTTAGATTATAGGTTAACATACTTGTGAAAATAC TTG
ATGT GTTTAAAGCCTGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTTATCCCCCT
 TTTAAAGTCATCCGTCTGGCTCAGGATTGGAGAGCTTGACCCACCAAAATGGCAAACA
 TCACCAGCTCCCAGATTGGACCAGTTGAAAGCTCCGAGTTGGGCCAGTTACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCCCTACAACACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTGACTTCAAATCTCACACCTGAGCCATCCC
 CAGTTCTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTCTCCTCCT
 CCTGGTTGGAGTCCTTCCCTCCAGGCAAAACTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTTGCAGCTCCAGCAGCACCATTGAAAATATCTGTGTCTG
 TCCACCAGCCACAGCCAAACACATCAAACCTGCTAACGGGGATACCCCCAGCTCTAAG
 ATCCCAGCTCTGCAGTGGAAATGCCTGGTCAGCAGATGTCACAGGATTAAATGTGCAGTT
 TGGGGCTCTGGAATTGGGT CAGAACCTCTCTCTGAATTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTGTATTGAAGTCTTAAGTGAGCCTTGAATACA
 TCTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCACACAAAGCCCTGTGAGTCATCAGAGTCAGCTCCA
 GGAACCACATCATGAATGGACATGGGGTGGTCAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTGTCTGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAAAACACCAGTTGGCAATGGCTATTCTGTTAACCACAGCAAGAAGGGAGGT
 TTTGGACCAGGTGTTGGCTGGTATTAGAAATGTCTTAACCACAGCAAGAAGGGAGGT
 GGTGGTCTCATATTCTCTGCCCTAATCAGACTGCACCACAGTCAGCAGTACAGTATGCAT
 TTTAAAGATGCTGGCCAGGCGGGTGGCTGATGCCATAATCCCAGTGCTTGGGGGCC
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC
 TGTCTCTACTAAAATACGAAAAACTAGCCGGTGTGGTGGCGCGCGTGCCTGTAATCCCAG
 CTACTTGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGEAPPKMANITSSQILDQLKAPSLGQFTTP
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSESAP
GTIMNGHGGGRSQQTLD SKYSSKLLSWLVPTKQRKRIAHVMWKT PVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCTGGGCTGGCGGGGCCATGGCGCTGCCATCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGCTGTACACCTGCAACCTGCACCACATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCACCCCGCGCTTGACCTGCGTAACCGCGGGCACGTGT
 GGACCGACCGGACGTGGAGGAGGCTAACAGGTGGTGCACGGGACCGGCAGCCGCCGG
 GTCCCGCACGACC CGCGGGACCGCCTGCTGGACCTCTACGCGTCGGCGAGCGCCGCGCCTA
 CGGGCCCCTTTCTGCGCGACCGCGTGGCTGTGGCGCGGATGCCTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCCGTCTTCCACCTGACGGTCGCCAACCCCACGC
 GGAGCCGCCCCCCCAGGGCTCTCCGGCAACGGCTCCAGCCACAGCGCGCCCAGGCCAG
 ACCCCACACTGGCGCGGGCCACAACGTATCAATGTCATCGTCCCCGAGAGCCGAGCCCAC
 TTCTCCAGCAGCTGGCTACGTGCTGGCACCGCTGCTGCTTCACTGCTACTGGTCAC
 TGTCCCTGGCCGCCCGCAGCGCCCGAGGCTACGAATACTCGGACCAGAAGTCGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCCACAGCCCCCTGCCGCCAAGTACATCGACCTAGACAAAGGGTCCGGAAGGAGAACT
 GCAAATAGGGAGGCCCTGGCTCCTGGCTGGCCAGCAGCTGCACCTCTCCTGTCTGCTC
 CTCGGGCATCTCCTGATGCTCCGGGCTCACCCCCCTCCAGCGCTGGTCCCGCTTCC
 GGAATTGGCCTGGCGTATGCAGAGGCCCTCCACACCCCTCCCCAGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCCGCCCTTGCTCACGGGTGGCCCTGCCACCCCTGGCACACC
 AAAATCCACTGATGCCCATCATGCCCTCAGACCCCTCTGGCTCTGCCGCTGGGGCCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAATGGGGTCAGCCTCA
 GGGCAGGAGTCCACTCCTCCAGGGCTCTGCTCGTCCGGGCTGGAGATGTTCTGGAGGA
 GGACACTCCCACAGAACATTGGCAGCCTGAAGTTGGGTCAAGCTGCCAGGAGTCCACT
 CCTCCTGGGTGCTGCCACCAAGAGCTCCCCACCTGTACCACTGCTCCTGTGTTG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTGCTCCTGTGTTG
 CTTTGGCCACCTGGGCTGCACCCCTGCCCTTCTGCCCATCCCTACCCCTAGCCTG
 CTCTCAGCCACCTTGATAGTCACTGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCCCT
 GGACTCTGCCTGGCTGGAGTCTAGGGCTGGGCTACATTGGCTCTGTACTGGCTGAGGA
 CAGGGAGGGAGTGAAGTTGGTTGGGTGGCTGTGTTGCCACTCTCAGCACCCACATT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGCCCCATCTGATTTAAAAAAAAAA
 AAAAAA

FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVALGAPALLTCVNRGHVWTDRHVEEAQQVVHWRDQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADAERGDFSLRIEPEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPRGSPNGSSHSGAPGPDP TLARGHNINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGDVNLA EFAVAAGDQMLYRSEDIQLDYKN
NILKERELAHSPLPAKYIDL DKGFRKENCK
```

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGCGTGGCGCAGCGCGAC**ATG**GCCGTTGTCAGAGGACGACTT
 CAGCACAGTTCAAACCTCACCGAACACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCGCCCTGGCCTGCAGAGGCCGAGGACCGCTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGCATTGGCAGTCTACTGCCATGAACTTCTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCGCAACTCCTCCAGCCCAGCACCAGGG
 GGACCTGAGGGCTCAGACATCCTGAACACTTTGAGAGCTACCTGCCGTGCGCTCACCG
 TGCCCTCATGCTGTGCTGGCAACTCCTGCTGTCAACAGGGTTGCAGTCCACATC
 CGTGTCTGGCCTCACTGACGGTCATCCTGGCCATCTCATGGTATAACTGCACTGGTGA
 GGTGGACACTCCCTCCTGGACCCGTGGTTTTGCCGTACCATTGTCATGGTGA
 TCAGCGGTGCCCACTGCTTCAGCAGCAGCATCAGGCATGACGGCTCCTTCTATG
 AGGAACCTCCAAGCACTGATATCAGGAGGAGCCATGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGGTGGACTGGCTGCATCCAGTGTGAGGAACAGCGCCCTGGCCTTCTCCTGACGG
 CCACCATCTCCCTCGTGCATGGACTCTACCTGCTGTCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCCTGTTCTGGGCCATGTGTTCTGGTGAAGAGGAGCTCCCCA
 GGACTCCCTCAGTGCCCTCGGTGGCCTCCAGATTCAATTGATTCCCACACACCCCCCTC
 GCCCCATCCTGAAGAAGACGCCAGCCTGGCTTGTGTACACCTACGTCTTCATCACC
 AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTGGGCTCACT
 GTGGACCACCAAGTTTCATCCCCCTCACTACCTCCTGTCAGTACAACATTGCTGACCTAT
 GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCAACAGCAAGGCCTCCAGGG
 TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTCGTGCTGTAACTACCAGCCCCGGT
 CCACCTGAAGACTGTGGCTTCCAGTCGATGTGATCCCCGACTCCTCAGCTCCCTGCTGG
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCTACGGGCTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGTGCTTTATGTGCTTGGGCTAACACTGGG
 CTCAGCCTGCTTACCCCTGGTGCACCTCAT**TAG**AAGGGAGGACACAAGGACATTGGT
 CTTCAGAGCCTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC
 TAAAGTTCACTGGGACAGAGAGCAGACACTCGGGCTCATCCCTCCAAAGATGCCA
 GTGAGGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAAACAGAACACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGTACTCCCTCACAGCTGATGGTTA
 ACATTCACCTCTTCTAGCCCTCAAAGATGCTGCCAGTGTGCGCCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTTTGCAACCTCCAGCTGCGCTCATTCCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCCTTACCCCTGAAGGGTCTCCCTGGAATGGA
 AGTCCCCTGGCATGGTCAGTCCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCAGGGTGAACAACTGCCACTAACCAAGACTGGAAAACCCAGAAAGATGGGCTTCCATGAAT
 GCTTCATTCCAGAGGGACCAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCAGGCTGGG
 TTTCAAAAAAAGAGGGATCCTCATGACCTGGTGTATGGCCTGGGCAAGATGAGGGTC
 TTTCAGTGTCCCTGTTACAACATGTCAAAGCCATTGGTCAAGGGCGTAATAAAACTTGC
 GTATTCAAAAA

FIGURE 48

MAVVSEDDFQHSSNSTYGTTS defense protein
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLA
VASTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCM
VILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALA
AFFLTATIFLVLCMGLY
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLSAPSVASRFIDSHTP
PLRPILKKTASLG
CVTYVFFITSЛИYPAVCTNIESLNKGSGSLWTTKFFIPLTTFL
LYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYP
ALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA
 TCTCCCACCGAGAGTCATGCCCCATTGCCCTGCACCTCCCTCGTCCTCGTCCCCATCCCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCC
 GAAGCCCCAGAGGGTATTGTGGTGGCGCTGGTGTGGCCGGCTGGTGGCCGCAAGGTGC
 TCAGCGATGCTGGACACAAGGTACCACATCCTGGAGGCAGATAAACAGGATCGGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGAGCTGGAGCCATGCGCATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTCAACCTGACCAAGTTACCC
 AGTACCGACAAGAACACGTGGACGGAGGTGACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCGAGAAGCTGGCTACGCCCTCGTCCCCAGGAAAAGGGCCACTGCCCGAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGCTGCAGAAAGG
 CGATGAAGAAGTTGAAAGGCACACGCTTGGAAATATCTCTGGGGAGGGAACCTGAGC
 CGGCCGGCCGTGCAGCTCTGGAGACGTGATGTCCGAGGATGGCTTCTATCTCAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCCTAGCGACAGACTCCAGTACAGCCGATCGTGG
 GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGTCCGGCTTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCACGTGGTGCTGCTGACGGCGAGCGGACCG
 CGGTGAAGCGCATCACCTCTGCCGCCGTGCCACATGCAGGAGGCCTGCGGAGG
 CTGCACTACGTGCCGCCACCAAGGTGTTCTAAGCTCCGCAGGCCCTCTGGCGCGAGGA
 GCACATTGAAGGCCACTCAAACACCGATGCCCGTCGCGCATGATTTCTACCCGCCGC
 CGCGCAGGGCGCGCTGCTGCCCTCGTACACGTGGTCGGACGCCGGCAGCGTTCGCC
 GGCTTGAGCCGGGAAGAGGCCTGGCGCTCGACGACGTGGCGCATTGCACGGGCC
 TGCGTGCAGCTCTGGACGGCACCGCGCTCGTAAGCGTTGGCGGAGGACAGCACA
 GCCAGGGTGGCTTGTGGTACAGCCGCCGGCTCTGGCAAACCGAAAAGGATGACTGGACG
 GTCCCTTATGCCGCATCTACTTGCCTGGCGAGCACACGCCCTACCGCACGGCTGGTGG
 GACGGCGGTCAAGTCGGCGCTGCGCGCCATCAAGATCAACAGCCGAAGGGCCTGCAT
 CGGACACGCCAGCCCCAGGGGACGCATCTGACATGGAGGGCAGGGCATGTGCATGG
 GTGGCCAGCAGCCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG
 CCAGTTATCTCCAAAACACGACCCACACGAGGACCTCGCATTAAAGTATTTCGGAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHQIETSPPARNL
KVLKADVVLLTASGPRAVKRITFSPPPLRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLASYTWSDAAAAFAGLSREEARLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTS

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTCTGCCTGC**AT**
GGACGCTCTGAAGCCACCCCTGTCTCTGGAGGAACCACAGCGAGGGAAAGAAGGGACAGGGACTCGTGTGGCAGGAA
 GAACTCAGAGCGGGAGCCCCCATTCACTAGAACCACTGAGAGATGCGGCCCCCTCCAGGGCTCTGAATTTCCT
 GCTGCTGTTCACAAAGATGCTTTTATCTTAACCTTTGTTTCTCCACTTCCGACCCGGCCTTGATCTGCAT
 CCTGACATTGGAGCTGCCATCTTCTGTGGCTGATCACCAAGACCTCAACCCGTCTTACCTCTTGACCTGAA
 CAATCAGTCTGTGGAATTGAGGGAGGAGCACGGAAGGGGTTTCCCAGAAGAACAAATGACCTAACAAAGTTGCTG
 CTTCTCAGATGCCAACACTATGTATGAGGTTTCAAAGAGGACTCGCTGTGACAAATGGCCCTGCTGGG
 ATATAGAAAACCAACCAGCCTACAGATGGCTATCTACAAACAGGTGCTGATAGAGCAGAGTACCTGGGTT
 CTGTCTTGTGATAAAAGTTATAAATCATCACCAGACCAGTTGTGGCATCTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCGAATTGGCTGTTACACGTACTCTATGGTAGCTGTACCTCTGATGACACCTTGGGACCAGAAC
 CATCGTACATATTGTCACAACAGGCTGATATGCCATGGTGTGACACACCCAAAAGGCATTGGTGTGAT
 AGGGAATGTAGAGAAAAGGCTCACCCGAGGCTGAAGGTGATCATCCTATGGACCCCTTGATGATGACCTGAA
 GCAAAGAGGGGAGAAGAGTGGATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTCAG
 AAAACCTGTGCCTCCTAGCCCAGAACGACTGAGCCTGAGCTCATCTGCTTCACCAGTGGGACCACAGGTGACCCAAAGG
 AGCCATGATAACCCATCAAATATTGTTCAAATGCTGCTGCCCTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTGGCATATCCTACCTCCCTGGCTCATATGTTGAGAGGATGTAAGGCTGTTGTGTA
 CAGCTGAGGCCAGAGTTGGATTCTTCCAAGGGGATATCGGTTGCTGGCTGAGCAGTGAAGACTTTGAAGCC
 CACATTGTTCCCGGGTGCCTCGACTCTAACAGGATCTACGATAAGGTCAAAGAGCACCCTT
 GAAGAAGTTCTTGTGAGCTGGCTGTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGATGATAG
 TTTCTGGGACAAGCTCATCTTGCAAAAGTCCAGGACAGCCTGGGGGAAGGGTCTGGTAATTGTCAGTGGAGC
 TGCCCCATGTCCACTTCAGTCATGACATTCTCCGGCAGCAATGGGATGTCAGGTGATGAGCTTATGGTCA
 AACAGAATGCACAGGTGGCTGACATTACATTACCTGGGACTGGACATCAGTCACGTTGGGTGCCCCCTGGC
 TTGCAATTACGTGAGCTGGAGATGTGGCTGACATGAACTACTTTACAGTGAATAATGAAGGGAGGGTCTGCAT
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCCTGAGAAGACACAGGAAGGCCCTGGACAGTGTGGCTG
 GCTTCACACAGGAGACATTGGCGTGGCTCCGAATGGAACCTGAAAGATCATCGACCGTAAAAAGAACATT
 CAAGCTGGCCAAGGAGAACATTCAGGAGAACATTCAGGAGAACATTCAGGAGTCAACCAGTGTAA
 AATTGTTGTACACGGGGAGAGCTACGGTCATCTTACTAGGAGTGGTGGTCTGACACAGATGTAACCTCC
 ATTTGCAGCCAAGCTGGGTGAGGGCTCTTGAGGAACCTGTCACAGTGTAAAGGGAGCCATT
 AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCCTAAAACCTTGAACAGGTCAAAGCCATTTCATCC
 AGAGCCATTTCATTGACAGCCTGTTGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCACTG
 TGCACGTGTTGTGAGAAAATTGGATAAAACATTCTTACATTGTTTGCCTTCTCTTATTTTTTAACC
 TGTTAAACTCTAAAGCCATAGCTTGTGTTTATATTGAGACATATAATGTGTAAACTTAGTCCCAAATAATCA
 ATCCCTGTTCCCATCTCGATGTTGCTAATATTAAAGGCTCAGGGCTACTTTATCAACATGCTGTCTCAA
 GATCCCAGTTATGTTCTGTGCTTCCCATGATTCCAACCTTAATACTATTAGTAACCAAGCTCAAGGGT
 CAAAGGGACCCCTGTGCTTCTCTTTGTTGTGATAAACATAACTGCCAACAGTCTATGCTTATTACA
 TCTTCTACTGTTCAAACACTAACAGAGATTTTAAATTCTGAAAACCTGCTTACATTGATTTCTAGCCACTCCAC
 AAACCACTAAAATTAGTTAGCCTACACTCATGTCATCATATCTATGAGACAAATGTCCTCGATGCTCTT
 CTGCGTAAATTAAATTGTGACTGAAGGGAAAAGTTGATCATACCAACATTCTCAAACACTCTAGTTAGATA
 TCTGACTTGGGAGTATTAAAATTGGGTCTATGACATACTGTCCAAAGGAATGCTGTCTTAAAGCATTATTTA
 CAGTAGGAACACTGGGAGTAAATCTGTTCCCTACAGTTGCTGCTGAGCTGAGCTGTGGGGGAAGGGAGTTGACA
 GGTGGGCCAGTGAACCTTCCAGTAAATGAAGCAAGCACTGAATAAAACCTCTGAACGGAAACAAAGATCT
 ACAGGCAAGCAAGATGCCACACAAACAGGCTTATTCTGTGAGGAACCAACTGATCTCCCCACCCCTGGATT
 AGAGTTCTGCTCACCTACCCACAGATAACACATGTTGTTCTACTTGTAAATGTAAAGTCTTAAAATAAC
 TATTACAGATAAAAAAA

FIGURE 52

```
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<MW: 82263, pI: 7.55, NX(S/T): 3
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CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVDRAEYLGSCLLHKGYKSS
PDQFVGIFQAQNRPWEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLKCVEHAYEPTPDDVAISYLPALAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLRNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELOKGIIRHDSFWDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVMFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHGVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPPEKTQEALDSDGWLHTGDIGRWLPGNTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLIQIFVHGESLRSSLGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAIILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLPTLKAKRGELSKYFRTQIDSPLYEHIQD
```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGGCGGAGGCCGCGCGAGCCGGCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCCGGGGCCCCTAAGCCATTCTGAAGTCATGGGCTGGCAGGACATTGGTGACCCGCCAAT
CCGGTATGGACGACTGGAAGCCCAGCCCCCATCAAGCCTTGGGCTCGGAAGAACGG
 AGCTGGTACCTTACCTGGAAGTATAAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGCCGTGCTTCTGCTGGTACTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG
 AGGCCGGGAGCAGGGCCGGGCATCCATGTCATTGTCCTCAACCAGGCCACGGCACGTG
 ATGGCAAAACGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTATTCT
 CAACATGGTAGCGCCCGGCCAGTGCTCATCTGCACTGTCAAGGATGAGGCCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGCAGCCAGGCTGCCCTGCCCTGGC
 TGGAGGGACACATGGGCCCTCGTGGACGAAAAGGAGGTCTGTCTCGGGAGAAAACATTC
 TAAGTCACCTGCCCTCTTCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGGCAGAGTGCCACTGGCAGACACAGAGCTGAACCGTCGCCGGCGC
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCCGTGGCTGTCTGCAG
 GGAACCGACCCAAATTACCTGTACAGGATGCTGCGCTCTGCTTCAAGGCCAGGGGTGTCT
 CCTCAGATGATAACAGTTTCTTCAAGGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
 GTTGGTCTGAGGGGCATCCAGCATCTCCATCAGCATCAAGAATGCCCGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTCAGTTCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTGCCTGGAATGACCAGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCCTGGCTGGCTGGCTC
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCTGAACAAACGCCGGGGCCGAGAGTGCATCATCCCTGACG
 TTTCCGATCCTACCACTTGGCATCGTCGGCCTAACATGAATGGTACTTACGAGGCC
 TACTTCAAGAAGCACAAGTTAACACGGTCCAGGTGTCCAGGCAATGTGGACAGTCT
 GAAGAAAGAAGCTTATGAAGTGGAAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCTTGTGAAGACTCTTCTGCCAGACACAGAGGCCACACCTACGTGGCC
 TTTATTCAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTGCCAAGTGCTCCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATGGGCCCTGGAGATTGTTCTGGAAGAAGA
 ACCACCTCCTGGTGGTGGGGTCCCGCTCCCCCTACTCAGTGAAGAAGGCCACCCCTCAGTC
 ACCCCAAATTCTGGAGCCACCCCCAACAGGAGGAGGGAGCCCCAGGAGGCCAGAACAGAC
ATGAGACCTCCAGGACCTGCCGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTGTAGATGCTGGTAGGGGCTGGGCTACCTGTTTAACA
 TGAGACTTAATTACTAACCAAGGGGAGGGTTCCCTGCTCCAACACCCGTTCTGAGTT
 AAAAGTCTATTATTAATTACTCCTTGTGGAGAACGGCAGGAGAGTACCTGGGAATCATTACG
 ATCCCTAGCAGCTCATCCTGCCCTTGAATACCCCACTTCCAGGCTGGCTCAGAACATCTA
 ACCTATTATTGACTGCTCTGAGGGCCTGAAAACAGGCCAACCTGGAGGGCCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTTACTCAGGAAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCTTA
 GACACTGGACCAGGCCTCTCAGCCTCTTGTCCAGATTCCAAAGCTGGATAAGTT
 GGTCAATTGATTAAGGAGAACCCCTGGAAAAA

FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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REQGRGIHVIVLNQATGHVMAKRVFDTYSPEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRLLLLFC SKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNPVAVIAGN
RPNYLYRMLRSILLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFP EAKFAVVLEEDLDIAV DFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSLKKEAYEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDL DVGNHRGLWRLFRKKNH
FLVVGVVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGACGCGTGGGTGCTGGAGGGCTAAAGAACCTGGAAAGGCCACTCTTGAACCACAC
CTGTTAAAGAACCTAAGCACCATTAAGCCACTGGAAATTGTTGCTAGGGTGTGGTGAATA
AAGGAGGGCAGAATGGGATTTCATCTCCATTAGCCTGCTCTGGCTATGTTGGGATGTTA
CGTGGCGGAATCATTCCTGGCTTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTTGG
GTGCTGGCCTCTGTGGAACTGCTCTGGCAGTCATCGCCTGAAGGGACTACATGCCCTTATGAA
GATATTCTTGAGGGAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAAAGCAGC
AGAAAAATCAGTTGTCATGACATGAGCACGCCACACAGCTGCATGCCATATTGGTG
TTTCCCTCGTTCTGGGCTCGTTTACATGTTGCTGGGACAGATTGTAACCTCCATGTGCATCT
ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAATCACCACCGCTGGTCTGGTTGTC
TGCTGCAGCTGATGGTGTGCTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
TGTTTGGCAATCATGTCACATAAGGCACCAGCTGCTTTGGACTGGTTCTTGTATGCATGCT
GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTGCATTGGCAGCACAGTTATGTC
GGTGCACATACTTAGGACTGAGTAAGAGCAGTAAGAAGCCCTTCAGAGGTGAACGCCACGGAGTGG
CCATGCTTTCTGCCCCGACATTCTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA
ATAGGGCACAGCCACAAGCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCTGGAAGTGGCAGCCT
GGTTCTGGGTTGCCATCCCTCATCCTGTCAGTAGGACACCAGCATTAAATGTTCAAGGTCCAGC
CTTGGTCCAGGGCCGTTGCCATCCAGTGAGAACAGCCGGACGTGACAGCTACTCACTCCTCAGTC
TCTTGTCTCACCTGCGCATCTACATGTATTCTAGAGTCCAGAGGGGAGGGTGAAGGTTAAAACCTG
AGTAATGGAAAAGCTTTAGAGTAGAACACATTACGTGCAAGTTAGCTATAGACATCCCATTG
TATCTTTAAAAGGCCCTGACATTGCGTTAATATTCTCTTAACCTATTCTCAGGGAGATG
GAATTAGTTAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGAATTGAAAATACAGT
GTTCTGTAATTAAAGCTATGCTCTTCTTAGTTAGAGGCTGCTACTTTATCCATTGATT
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TAAACAGCTCCTTGGCACGTGCCATTCCATCAAATGGAGCAGGGAGG
TGGGAGGAGCTCTAAAGAGGTGACTGGTATTGTTGATGCAATTCTCCTTGCAGAAT
ACCTGTCCTCCACATTCTAGAGGAGGCCAAGTTCTAGTTCACTTAGGCTTCTTCAAGAA
CAGTCAGATCACAAGTGTCTTGGAAATTAAAGGGATATAAATTAAAGTGAATTGGATGGTTAT
TGATATCTTGTAGCTTAAAGACTACCAAAATGTATGGTGTCTTCTTGTCTTCTA
TTTTTTTTAATTATTCTCTAGCAGATCAGCAATTCCCTAGGGACCTAAATACTAGGT
GGCGACACTGTGCTTCTCACATAACCACCTGCTAGCAAGATGGATCATAATGAGAAGTGT
TTGATTAAAGCTATTGGAATCATGCTCTGTCTTGTCTTGTCTTCTTCTA
TCCCTCTAGCCTCCTGCCACAATTGCTGCTACTGCTGGTAAATTGTTG
CTTATCAGGACAACCACTCTGAACTGTAATAATGAAGATAATAATCTTATTCTTATCCCCT
CAAAGAAATTACCTTGTCAAATGCCGTTGAGCCCTTAAATACCACCTCCTATGT
ATTGACACAACTACTAATCTGTAATTAAACAAATTGAGATAGCAAAAGT
TTAACAGACTAGGATA
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GACTGGTGTGAGACTTGAGGTTCTAGTCCTTCAAACACTATATGGTGC
TAGATTCTCTGGA
AACTGACTTGTCAAATAAGCAGATTGTAAGTGT
AAAAAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVVDQ
IGNSHVHSTDDPEAARSSNSKITTLGLVVHAAADGVALGAAASTSQTSQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGCGGCCTCGTAGGGGCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTGAG**ATGA**TGGCTTGG
 GAAACGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTGGCTTCAACTACTGGATTGCGAGCTCCGGAGCGTGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCACAAGCTGTACCAGGACGAAAAGGCGGTTTGGTGA
 TAACATCACACAGGTGAGAGGCTCATCCGAGTGCAAGACCAGTTCAAAGACCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAAAGAACAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCCCTGCCACACACAGAGGTGCCACAAGGGAAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGGTTGGATTCAAAGAGACAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGGCTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTGTCACTCCCCGACGGACAGGAGGAGCAGGAAGCT
 GCCGGGAAAGGGAGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAAATGACAGAAACATAGATG
 TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTACTTGATCAGCGTGAAAAGCGG
 AATCATACACT**TGA**ATTGAACTGGAATCACATATTCACAAACAGGGCGAAGAGATGACTA
 TAAAATGTTCATGAGGGACTGAATACTGAAATGTACTAAATAATGTACATCTGA

FIGURE 58

MMGLGNGRRSMKSPPVLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLQYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEPQPRILQAAGLPHTEVPGKGNVLGNSKSQTPAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEKGREGFGGAGELGQTPOVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNDENEAESETDKQAALAGND
RNIDVFVNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29

FIGURE 59

GGATGCAGAAAGCCTCAGTGTGCTCTTCCTGGCCTGGGTCTGCTTCCTCTACGCTGGCATTGCCCTCTTCA
 CCAGTGGCTTCCTGCTCACCGTTGGAGCTACCAACCATAAGCAGCTGCAAGAGCCCCCAGGCCCTGGTCCC
 TGCCATGGGGAGCCAAGGAAACCTGGGCTGCTGGATGGCTTCCGATTTCGCGGGTTGTGTTGGTGTGA
 TAGATGCTCTGCGATTGACTTCGCCCAGCCCCAGATTACACAGTGCCTAGAGAGCCTCTGTCCTCCCTACCC
 TCCTGGCAAACTAAGCTCCTGAGAGATCCTGGAGATTCAAGCCCACCATGCCGCTCTACCGATCTCAGG
 TTGACCCCTCCTACCACCACCATGCAGCGCTCAAGGCCCTCACCACTGGCTACTGCTACCTTATTGATGCTG
 GTAGTAACCTGCCAGGCCACGCCATAGTGAAGACAATCTCATTAAGCAGTCAACCAGTGCAGGAAGCGTAG
 TCTTCATGGAGATGATACCTGAAAGACCTTTCCCTGGTCTTCTCAAAGCTTCTTCTCCATCCTTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG
 ACGTGCTGATTGCTCACTTCTGGGTGGACACTGTGGCCACAAGCATGGCCTCACCAACCTGAAATGCCA
 AGAAAATAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
 CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTTTC
 TGTATAGCCCCACAGCAGTCTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTGTGC
 CCACGCTGGCCCTGCTGCTGGCCTGCCATCCATTGGGAATATCGGGAAAGTGTGGCTGAGCTATTCTCAG
 GGGGTGAGGACTCCAGCCCCACTCCTCTGCTTAGCCAAGCCTCAGCTCTCATCTCAATGCTCAGCAGGTGT
 CCCGATTCTCATACCTACTCAGCTGACTCAGGACCTCAAGCTAACGGAGCTTCAGCTGCAGAACCTCT
 TCTCCAAGGCCTCTGCTGACTACCAGTGGCTTCTCAGAGGCCAACGGGAGCTGAGGGCAGACTGCCGACTGTGA
 TTGCTGAGCTGCAGCAGTCTCTGCGGGAGCTGGCATGTGCAGTCTGGGCTCGTTCTCTGTGTC
 GCATGGCGGGGGTACTGCTCTTGTGCTCTGCTTATCTGCCTGTCAGTGGCAATATCCC
 CAGGCTTCCATTCTGCCCTACTCTGACACCTGTGGCTGGGCTGGGCTGGTGGGGCATAGCGTATGCTGGAC
 TCCTGGGAACTATTGAGCTAGATCTAGTGCCTCTAGGGCTGTGGCTGAGCTCATTCCCTCCCT
 TTCTGTGAAAGCTGGCTGGCTGGGGCTCCAAGAGGCCCTGGCAACCCCTGTTCCCATCCCTGGGCCGTCC
 TGTTACTCTGCTGTTCGCTGGCTGTGTTCTCTGATAGTTGTTAGCTGAGGCCAGGGCCACCCCT
 TCCTTTGGGCTATTCATCTGCTCTGGTGTCCAGCTCACTGGAGGGCCAGCTGCTCCACCTAACGTAC
 TCACAATGCCCGCCTGGCAGCATTGACACAAACAAACCCCCAACGGCACAATGGTCATATGCCCTGAGGCTTG
 GAATTGGGTTGCTTTATGTACAAGGCTAGCTGGCTTTTCATCGTTGCCCTGAAGAGACACCTGTTGCCACT
 CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTCAGGCCAAGAATTATGGTATGGAGCTGTG
 CGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTCGCCTATGGTAATCTAACAGGCCAGGCC
 CCATGCTCTTGTGCGTGGGACTGCCCTAATGCCATTGGTACTGCTGCCTACTGGCATTGGCGTCGGGG
 CAGATGAGGCTCCCCCCCCTCCTGGCTCTGGTCTCTGGGATCCATGGTACTGCTGCCCTGGCTGTAGCAGGG
 TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGGACTGTGACAGTGTGGCTGAAGGCTGGGAGGCC
 GGACCAAGACTGCTCTCAGCCCTCTCAGGGCCCCACTCTCAAGCTGACTTGGATTATGTGGTCCCTCAA
 TCTACCGACACATGCAGGAGGAGTCCGGGGCGGTAGAGAGGACCAATCTCAGGGTCCCTGACTGTGGCTG
 CTTATCAGTTGGGAGTGTACTCAGCTGCTATGGTACAGGCCCTCACCTGTTGGCCTTCCACTTCTGCTGT
 TGCATGCGGAGCGCATCAGCCTGTTGCTCTGCTCTGCTGAGAGCTCTCTCTACATCTGCTTGCTG
 CTGGGATACCGTCACCAACCCCTGGCTTACTGTCCTGCATGGCAGGAGCTCTGGCTGGGCCCTCATGCCA
 AACAGACCTCTACTCCACAGGCCACCAGCCTGCTTCCAGCCTATGGCATGCAGCCTCTGTTGGATTCC
 CAGAGGGCATGGCTCTGACTTGGCTGCCCTTGCTAGGGAGCCAACACCTTGCCTCCACCTCTCT
 TTGCACTAGGGTGTGCTGCTCTGGCTCTGGCTCTGGCTTCTGTGAGAGTCAAGGGCTGCCAGAGACAGCAGC
 CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGGAGAGGAGGCCACTGATGGAGATGCCCTGGGG
 ATGCCCTCAGCACTCTATGCACTGCTGCAGCTGGGCTCAAGTACCTTCTTATCTTGTGATTCA
 TGGCCTGTCCTGGCAGCCTCCATCTCGCAGGCATCTCATGGTCTGGAAAGTGTGTTGCCCTAAGTTCATAT
 TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCTGGGCTAGCTTGTGATGAGAGTGGATGGT
 CTGTGAGCTCTGGGCTCAGGCAGCTATTCTGGCCAGAGGTTAGCCTAGTGTGATTACTGCCACTTG
 ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCTGACAGTACTGGATGATCTGCAAGACAGGCCAGTGGAGTA
 TGATCCCTAACTCTGATTGGATGCACTTGAGGGACAAGGGGGCGGTCTCGAAGTGGAAATAAAATAGGCC
 GCGTGGTGAATTGCACTTATAATCCCAGCAGTGGGAGGAGGAGGATTGCTTGGTCCAGGAGTTCA
 AGACCAGCCTGTGGAACATAACAAGACCCGCTCTACTATTAAAAAAAGTGTAAATAAAATGATAATAT

FIGURE 60

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
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MASRFSRVVLVLIDALRFDFAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLF
PGAFSKAFFFPSFNVRDLDLTVNDGILEHLYPTMDSGEWDVLIAHFLGVDHCGKHGPHEPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAALFLYSPAVFPST
PPEEPEVIPQVSLVPTLALLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRLFHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAYSSFLPFLWKAWAGWGSKRPLATLFFPIPgpVLLLLFRLA
VFFSDSFVVAEARATPFLGSFILLVVQLHWEGQLLPPKLLTMRPLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
RAVAGLAASGLALLLWKPVTLVKAGAGAPRTRTVLTPTSGPPTSQADLDYVVPQIYRHMQE
EFRGRILERTKSQGPLTVAAAYQLGSVYSAAMVTALTILLAFPLLLHAERISLVFLLLFIQSFL
LLHLLAAGIPVTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFILGIQILACALAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

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Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTCCTGGCGGCCTGGGACGGCAGTCCCTGT
 GTCTCTGGTGGTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**
 CCTACAATGGACTCCACCAGAGGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGBAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGACCAACCACGCTGGTCTCACCTGGCTGGAGCCGAACACTCTTACTGCGT
 ACACGTGGAGTCCTCGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTG
 CCAGGACTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTCTGGTATGTTG
 CCCATATCTATTACCGTGTTCCTTTCTGTGATGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTGATTTGATTGAAATGAATTGACAAAA
 GATTCTTGTGCCTGCTGAAAAAAATCGTGATTAACTTATCACCTCAATATCTGGATGAT
 TCTAAAATTCTCATCAGGATATGAGTTACTGGAAAAAGCAGTGATGTATCCAGCCTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGGAGGTGAAACATTAG
 GGTATGCTTCGCATTGATGAAATTGGACTCTGAAGAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCTCAGCAGAACATACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTGTCGGGGCCTGAAGAGCAGGAGCTCAGTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGCAGTCTGGGCCG
 CAAACGTTACAGTACTCATACACCCCTCAGCTCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGATCCCC
 AAACTGGCAGGCTGTGATTCTCGCTGTCAGCTCGACCAGGATTAGAGGGCTGCAG
 CCTTCTGAGGGGGATGGCTCGGAGAGGAGGGTCTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGT
 TATATGTGCAGATGGAAA**TGA**TGCCAACACTCCTTTGCCCTTGTGCAAAC
 AAGTGAGTCACCCCTTGATCCCAGCCATAAGTACCTGGATGAAAGAAGTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTG
 GTTCATGCATGTAGGTCTTAACAATGATGGTGGCCTCTGGAGTCCAGGGCTGGCCGGT
 TGTTCTATGCAGAGAAAGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTACAGG
 TGGGTGT

FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQ RVFKELKLLTLC SIS SQIGPPEVALTTDEKSISVVLT APEKWKRN PEDLPVSMQ
QI YSNLKYNV SVLNTKS NRTWSQC VTNH TLVLT WLE PNTLY CVH VES FVP GP PRRA QPSEKQ
CART LKDQS SEFKA KII IFW YVLP I SITVFL FSVM GY SIYRYI HVGKEKHPANL LILIYGNEFD
KRFFVPAEKIV INFITLN ISDDSKI SHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEE EVKH
LG YASHLMEIF C DSEEN TEGTS LTQQESLSRTI PPDKTVIEYEYDVRTTDICAGPEEQE SL
QEEVSTQGT LLESQA ALAVLG PQLQ YSYPQL QDPLA QEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPS LSSFDQDSEGCEPSEG DGLGEEGLL SRLYEE PAPDRP PGENET YLMQF MEEW
GLYVQ MEN
```

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACCGTGGCGGACCGTGGCGGACCGTGGGTCTCTGCAGGAGACGCCAGCCTGCG
 TCTGCCATGGGCTCGGTTGAGGGCTGGGACGTCTGCTGACTGTGGCACCGCCCT
 GATGCTGCCGTGAAGCCCCCGCAGGCTCTGGGGGCCAGATCATGGGGGCCACGAGG
 TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGCAACATCACTGCGGA
 GGCTCCTGCTGCGAGCCGCTGGTGGTCTGGCCGCCACTGCTTCAGCCACAGAGACCT
 CCGCACTGGCTGGTGGTCTGGCGCCACGTCTGAGTACTGCGGAGCCCACCCAGCAGG
 TGTTGGCATCGATGCTCTCACACGCACCCGACTACCACCCATGACCCACGCCAACGAC
 ATCTGCCTGCTGCGCTGAACGGCTCTGCTGTCTGGCCCTGCAGTGGGCTGCTGAGGCT
 GCCAGGGAGAAGGGCAGGCCACAGGGGACACGGTGCCGGTGGCTGGCTGGGCT
 TCGTGTCTGACTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
 CCGGACGTCTGCAACAGCTCCTGGAAGGGCACCTGACACTTACCATGCTCTGCACCCGCAG
 TGGGGACAGCCACAGACGGGCTTCTGCTCGGCCACTCCGGAGGGCCCTGGTGTGCAGGA
 ACCGGGCTCACGGCTCGTTCTCGGGCTCTGGTGCAGGCCACCCAAAGACCCCCGAC
 GTGTACACGCAGGTGTCCGCCTTGTGGCCTGGATCTGGACGTGGTCTGGCGAGCAGTCC
 CCAGCCGGCCCCCTGCCTGGACCACCAGGCCAGGAGAAGCCGCCTGAGCCACAACCT
 TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
 AAGCCTGATGTTCAAGGTTGGGTGGGACGGGAGCGGGTGGGCACACCCATTCCACATGCA
 AAGGGCAGAAGCAAACCCAGTAAAATGTTAAGTACGACAAAAAAAAAAAAAGAAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSGWAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLMCTRSGDHSRRGFCSADSGGPLVCRNRAHGLVSFGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCCGACTCCGGACGCCGTACGCCCTGA
 CGCCTGTCCCCGGCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG
 CAGGCGCCGCCGTGCTCAAGGACTATGTCACCGGTGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGGCACACAGGCATGGGAAGCAGACCGCCTT
 GGAACCTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGGGGAGACCCCTCAATACCATGTCAACGCCGGCACCTGGAC
 TTGGCTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAACAAACGCGGGTGTGATGCGGTGCCCTGGACCGAGGACGGCT
 TCGAGATGCAGTTGGCGTTAACCAACCTGGGTCACTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCTCGCGGATCATCAACCTCTCGTCCCTGGCCATGTTGCTGG
 GCACATAGACTTGTACGACTTGAACACTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTGCCATCGCCTCTCACCAAGGAGCTGAGCCGGGGCTGCAAGGCTCT
 GGTGTACTGTCAACGCCCTGCACCCCGCGTGGCCAGGACAGAGCTGGCAGACACACGGG
 CATCCATGGCTCCACCTCTCCAGCACCAACTCGGGCCATCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGCCGCCAGCCCAGCACATACCTGGCGTGGCGAGGAAGTGGCGGATGTT
 TCCGGAAAGTACTCGATGGACTCAAACAGAAAGGCCCGGCCCCGAGGCTGAGGATGAGGA
 GGTGGCCCGGAGGCTTGGCTGAAAGTGCCGCCTGGTGGCTTAGAGGCTCCCTGTGA
 GGGAGCAGCCCTCCCCAGA**TAA**CTCTGGAGCAGATTGAAAGCCAGGATGGCGCTCCAG
 ACCGAGGACAGCTGTCCGCCATGCCGCAGCTTCTGGCACTACCTGAGCCGGAGACCCAG
 GACTGGCGGCCATGCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTCCGTCTGCTCTGCTGCCAGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGCCGAGGAGGAAGGGGCTC
 TGTGCACCTGCAGGCCACGTCAAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTCCAAGGTGC
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTTGGTGGATTCTGGTCCCTGTGGACCT
 TGTGCATGCATGGCCTCTGAGCCTGGTTCTCAGCAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG
 GGTGTTGCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
 GAGTTCAGGCTCTGCACGGCATGGAGTGGAAACCCACCAGCTGCTGCTACAGGACCTGGGA
 TTGCCTGGACTCCCACCTTCTATCAATTCTCATGGTAGTCAAACACTGCAGACTCTCAAAC
 TTGCTCATTT

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLDKLASPKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSCLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLVAAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSvreQPLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTCGCGAGCGCTGGC**ATG**TGGTCTGGGCGCGCTGGCGCGCTGCTGGCGGTGCTG
 GCGCTCGGCACAGGAGACCCAGAAAGGGCTGCGGCTCGGGCGACACGTTCTCGCGCTGAC
 CAGCGTGGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGCTGAGGCGGTACCTGC
 GCAGGGAGGAGGCAGCGCTGCGGACACTGACTAGATTCTACGACAAGGTACTTCTTGAT
 GAGGATTCAACAAACCCCTGTGGCTAACCTCTGCTTGCAATTACTCTCATCAAACGCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCAGCCTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCGCTGCAGGACGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT
 TCAGAGAGTCAGTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCTATGACATGGGGGATTATTACCATGCC
 ATTCCATGGCTGGAGGAGGCTGTCAGTCTCTCCGAGGATCTACGGAGAGTGGAAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCTTTGCTTATTCCGGGAGGAA
 ATGTTCTGTTGCCCTCAGCCTCTCGGGAGTTCTCTACAGCCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTGAAATATGAAAGGCTTGGCAGAGAGCCCCAACACGTGGTAGC
 TGAGGCTGTCACTCAGAGGCCAATATAACCCACCTGCAGACCAGAGACACCTACGAGGGC
 TATGTCAGACCCCTGGTTCCCAGCCACTCTTACCCAGATCCCTAGCCTACTGTTCTAT
 GAGACCAATTCCAACGCCAACCTGCTGCTCCAGCCATCCGGAAAGGAGGTACCCACCTGGA
 GCCCTACATTGCTCTTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATTGCTGGCTGAAGGACACTGTTGACCCAAACTGGTGAACCTCAA
 CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCGGCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACTATGGCATCGGAGGACACTATGAGCCTCACTTGACCATGCTACGTACCAAGC
 AGCCCCCTTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCACAGCCTTACATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
 ATGCAGCACTGTTGGGAACCTGCACAGGAGTGGTAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCCTGTCCTGGTGGAGATAAGTGGTGGCAACAAGTGGATACATGAGTATGG
 ACAGGAATTCCGCAGACCCCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAC
 TGGTGGAGTCTGTGGCTTCCAGAGAAGGCCAGGAGCCAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCTGGAAAGAAGGCCCTGTCAGCTTGTCTGCCTCGCAAATCAGAGGC
 AAGGGAGAGGTTGTTACCAAGGGACACTGAGAACATGATCTGGGGCACGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAAGTTCTGG
 AGTTCAAGATACTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGGTC
 TTTGGCACTTGAACCTTGACCAACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCCAGAACATTAAAGACTTCTCCCCACTGCCTCTGCTGCAGCCCAAG
 CAGGGAGTGTCCCCCTCCAGAACGATATCCAGATGAGTGGTACATTATATAAGGATTTT
 TTTAAGTTGAAAACAACATTCTTTCTTTGTATGATGGTTTTAACACAGTCATTAAAA
 ATGTTATAAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSAVARALAPERRLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHQLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNRIAALTGLDVRPPYAELYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTAACGTCCTGCTCCATCTCAGGAGCCCCGTCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGAGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCGCGCGGGGAG
 CGCCCAGG**ATG**CCCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGTCT
 GTCTGTGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCCTGGCGTGTATGTTCATGGTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTATGTACATCCTGGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCGAGACCATTG
 ACTTCCTGAACGACAACATTGAAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA
 AACATCATGGACTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACGACACTGCAGTGCCCTGGACCCCTGGCTGTGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAAGTTGTAACACCATGTGTGGCTACAAACTATCGAC
 AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGCTGCACCAACGCCGTGATCAT
 CTGGTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGTGGAGGACATCATGGAGCAC
 TCTGTCACTGATGGCTCCTGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCAAAT**TAG**GGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCCTGTGTAGGTCCCACGGCCTCTGCCCTC
 CCCAGGGAGCAGGCCTGGCCTCCCTAACAGAGGTTTCCCCGAGGCAGCTCTGGAAATCTGT
 GCCCACCTGGGCCTGGGAACAAGGCCCTCCTTCTCCAGGCCTGGCTACAGGGAGGGA
 GAGCCTGAGGCTTGCTCAGGGCCATTTCATCTGGCAGTGCCTGGCGGTGGTATTCAA
 GGCAGTTTGTAACGACCTGTAATTGGGAGAGGGAGTGTGCCCTGGGGCAGGAGGGAAGG
 GCATCTGGGAAGGGCAGGAGGGAAGAGCTGTCATGCAGCCACGCCATGGCCAGGTTGGC
 CTCTTCTCAGCCTCCAGGTGCCTTGAGCCCTTGTGCAAGGGCGCTGCTTGTGAGCCTA
 GTTTTTTACGTGATTTGTAACATTCACTTTGTACAGATAACAGGAGTTCTGAC
 TAATCAAAGCTGGTATTCGGCATGTCTTATTCTGCGCCTTCCCCAACAGTTGTTAA
 TCAAACAATAAAACATGTTGTTGTTAAAAAAA

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYWLKFSLIIYSTVFWLIGALVLSVGIVAEVERQKYKTLESAFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGIENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIVVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPAGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGGCCGGCCGTGGACCTTCACCCCTCTGTGGTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAGGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGCCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAAGTGTATAAGCTCTCCTCCTGGTAACGCCCTAGCTAACGC
 AGGTCACTGAACCTCCTAGTGCCATCCCTGCCAATCTAGTGAAAAACCAGCTGTGTCCCCTG
 ATCGAGGCTTCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTAAGGTGCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTGACACCATTG
 AGCTCTACCTGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCACCCCTGGACAACATCCCCTCAGCCTCATCGTGAGTCA
 GGACGTGGTAAAGCTGCAGTGGCTGCTGTCTCTCCAGAAGAATTGATGGCCTGTTGG
 ACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATTGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTAAGATCCTAACTCAGGACACTCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCAACTGATCGTGCTGGAAGTGTGTTCCCTCCA
 GTGAAGCCCTCCGCCCTTGTTCACCCCTGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTAACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCAACAGAAATGGCAAATTAAAGATCTGGGTCCCAGTGTGATTGGT
 AAGGCCTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCC
 AGCCTCTGTGGAAACCCAGCTCTCCTGCTCCAGTGAAGACTGGATGGCAGCCATCAG
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTATAGACCATCCCTCTGCAAT
 CAATAAACACTTGCCTGTGAAAAAA

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGI PVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSIRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFnNSAASLTMP TLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVL
PESAHLRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKD ALVTPASLWKPSSPVSQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTTGGCGGTTTGGTGTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTGCGACGTCCCTCAGCCTCTGCCAAAGAAAGAAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACAGCATAGACAGTGTGTCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAACCTCTGGCGATACTCCAGTGCAATTACCAACAGGGATATTTTGCCATGGTGGATTGG
 ATGAAGGCTCTGATGTATTCAGATGCTAACATGAATTCACTGCTTCAACTTT
 CCTGCAAAAGGGAAACCCAAACGGGTGATACATATGAGTTACAGGTGCGGGGTTTCAGC
 T~~G~~AGCAGATTGCCCGGTGGATGCCGACAGAACTGATGTCAAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCTATGTTGGGATTGCTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTCGAAGAAGTAATATGGAATTCTCTTAATAAAACTGGATGGCTTGCAGCTTGTG
 TTTTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTGTA
 GCTGAAACACACATTGTTCTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGGCTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTTGTTGGCTGGTATTG
 GACTTGGTGTATTATTCTTCAGTGGATGCTCTATTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTCTGATGAGT**TAA**AAAGGTCCCAGAGATATAGACACTGGAGTACTGAA
 ATTGAAAAACGAAAATCGTGTGTTGAAAAGAAGAATGCAACTTGTATATTGTATTAC
 CTCTTTTTCAAGTGATTTAAATAGTTAATCATTAAACAAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTAACCTCTT
 CCCAGTGAACTTATGGAACATTAAATTAGTACAATTAAAGTATATTATAAAATTGTAAAA
 CTACTACTTGTGTTAGTTAGAACAAAGCTAAAACACTTTAGTTAACTTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCTTCTAGCTTCTCATCTTGTGTGGATGTGTAT
 ACTTTACGCATTTCTTTGAGTAGAGAAATTATGTGTGTCATGTGGTCTCTGAAAATG
 GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTCTCCTCCT
 GCATATTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGCTCAAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTCTGCTTGAGTATGGTGTAACTACCTGTATTAGAAA
 GATTTCAGATTCTTCCATCTCCTTAGTTCTTAAAGGTGACCCATCTGTGATAAAAATA
 TAGCTAGTGTAAAATCAGTGTAACTTATACATGGCCTAAAATGTTCTACAAATTAGAGT
 TTGTCACCTATTCCATTGTACCTAAGAGAAAAATTAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGAACCTACGCCTGTAATCTCAGCACCTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTCAAGGAGTTCGAGACCACATCTGGCCAACATGGTGAACACCCGTCCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKSQLMEWTNKRPVIRMNGDKFR
RLVKAPPNYSVIVMFALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPGRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEEFLFNKTGWAFAAALCFVLAATSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAATGCAAGCTTGGGAGTTGTCGCTGCCCTGCCCTGCTCTGCTAGGGAGA
 GAACGCCAGAGGGAGGCAGCGGCTGGCCCGGCCAGGCTCTCAGAACCGCTACCAGGCG**ATG**CTA
 CTGCTGTGGGTGCGGTGCGAGCCTGGCGCTGGCGACTGGCCCCGGAGCAGGGGA
 GCAGAGGCCGGAGAGCAGCCAAAGCGCCAATGTGGTGTGGCGTGAGCGACTCCTCGATG
 GAAGGTTAACATTCATCCAGGAAGTCAGGTAGTCAAACCTTCTTATCAACTTATGAAG
 ACACGTGGACTTCCTTCTGAATGCCTACACAAACTCTCCAAATTGTTGCCCCATCACGCGC
 AGCAATGTGGAGTGGCTCTCACTTAACAGAAATCTTGAATAATTAAAGGGTAG
 ATCCAAATTATAACACATGGATGGATGTATGGAGAGGCATGGCTACCGAACACAGAAATT
 GGGAAACTGGACTATACTCAGGACATCACTCCATTAGTAATCGTGTGGAAAGCGTGGACAAG
 AGATGTTGCTTCTTACTCAGACAAGAAGGCAGGCCATGGTTAATCTTATCCGTAAACAGGA
 CTAAAGTCAGAGTGATGGAAAGGGATTGGCAGAATACAGACAAAGCAGTAAACTGGTTAAGA
 AAGGAAGCAATTAAATTACACTGAACCATTGTTATTACTGGGATTAATTACACACACCC
 TTACCCCTCACCATCTTCTGGAGAAAATTGGATCTCAACATTACACATCTCTTATT
 GGCTTGAAAAAGTGTCTCATGATGCCATCAAAATCCAAAGTGGTCACCTTGTCAAGAAATG
 CACCCCTGTAGATTATTACTCTTCTTACACAAAAACTGCACGGAAAGATTACAAAAAAGA
 AATTAAGAATATTAGAGCATTATTATGCTATGTGTGCTGAGACAGATGCCATGCTGGTG
 AAATTATTGGCCCTTCATCAATTAGATCTTCTTCAAGAAAACATTGTCACTACCTCA
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTGATGATGGGACAGGAATTAAAGCCGGCTACAAGTATCAAATG
 TGGTTCTCTGTGGATATTACCTACCATGCTTGATATTGCTGGAATTCTCTGCCTCAG
 AACCTGAGTGGACTCTTGTGCGTTATCATCAGAAACATTAAAGAATGAACATAAAAGT
 CAAAAACCTGCATCCACCTGGATTCTGAGTGAATTCCATGGATGTAATGTGAATGCCTCCA
 CCTACATGCTTCGAACTAACCACTGGAAATATATAGCCTATCGGATGGTCATCAATTG
 CCTCAACTCTTGATCTTCTCGGATCCAGATGAATTAAACAAATGTTGCTGTAATTCTC
 AGAAATTACTTATTCTTGATCAGAAGCTCATTCCATTATAAAACTACCCTAAAGTTCTG
 CTTCTGTCCACCAGTATAATAAGAGCAGTTATCAAGTGGAAACAAAGTATAGGACAGAAT
 TATTCAAACGTATAGCAAATCTAGGTGGCACCAAGACTGGCAGAAGGAACCAAGGAAGTA
 TGAAAATGCAATTGATCAGTGGCTTAAACCCATATGAATCCAAGAGCAGT**TGA**ACAAAAA
 GTTTAAAAATAGTGTCTAGAGATACTATAAATATTACAAGATCATAATTATGTATT
 AAATGAAACAGTTTAATAATTACCAAGTTGGCCGGGCACAGTGGCTCACACCTGTAATC
 CCAGGACTTGGGAGGCTGAGGAAAGCAGATCACAAAGTCAGAGATGAGACCATCTGGC
 CAACATGGTGAACCCCTGTCTACTAAAAATACAAAATTAGCTGGCGGGTGGTCACA
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGAGCAGGAGATCGCTGAACCCGGGAGGCAGCAG
 TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTCG
 AAAAAAATAAAAATAATAATAATTACCAATTTCATTATTGTAAGAATGTAGTG
 TATTGTAAGATAAAATGCCAATGATTATAAAATCACATATTCAAAATGGTTATTATTA
 GGCCTTGTACAATTCTAACAAATTAGTGGAAAGTATCAAAGGATTGAAGCAAATACTGTA
 ACAGTTATGTTCTTAAATAATAGAGAATATAAAATTGTAATAATATGTATCATAAAAT
 AGTTGTATGTGAGCATTGATGGTGAaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
 aa

FIGURE 76

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
|<subunit 1 of 1, 536 aa, 1 stop
|<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVSDSFGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPsRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLRQEGRPMVNLI RNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHOLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELTVNAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMN PRAV

```

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
GCCTCTCTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTCTGGGGCTTTGGGCACACT
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG
CAGTTGGCTTCTCCAAGGGCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
TGTGACATCTATAGCACCCCTCTGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTGTGGTGGCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCGAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTC
ATCCTTGGAGGCCTCTGGATTCAATTCTGTTGCCTGGAATCTTCATGGATCCTACGGGA
CTTCTACTCACCCTGAGCTGACAGCATGAAATTGAGATTGGAGAGGCTCTTACTTGG
GCATTATTCTCCCTGTTCTCCCTGATACTGGAAATCATCCTCTGCTTTCTGCTCATCC
CAGAGAAATCGCTCCAACACTACGATGCCAACCAAGCCAAACCTCTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
ATGTGTGAAGAACCAAGGGCCAGAGCTGGGGGTGGCTGGTCTGTGAAAAAACAGTGGACAG
CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTCAGAAGGTGCTGCTGAGG
ATAGACTGACTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAACAGCATG
CAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTCTCACCTTGCTGCTC
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCCTAACGCCAGGACTCAGAGG
ATCCCTTGCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAACATCACATCCACTG
ACTGACCCCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTATTGCTGG
GGATGGGAAGGAGAAGCAGTGGCTTGTGGCATGCTCTAACCTACTTCTCAAGCTTCCC
TCCAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTGTTATGACTCCACAGTGTCC
AGACTAATTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

FIGURE 78

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLTIVAMLLPSWKTSSYVGASIVTAGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWNLHGILRDFYSPLVPSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV
```

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains: .

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCAGTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCCTCCTCTTGTGTCAGGGAAAGTCATCGCTCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTGAGCTCTGCTGTCTGATTCCCTTGGCCTCACAAACGATTGGTTG
TGAAGCTGAAGGTTCAAGGTGTGAATTCCAGTGCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTCCCTGAGAAGACATAGAAAAGAAATCAACTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAAGTAGAGAAGCCTGAGGAATTACAAATG
ATGCAGCTCCAAGCCATTGTATGGCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAAAGTGGTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYVSVC~~LLL~~C~~P~~REVIAPAGSEPWL~~C~~Q~~P~~APRCGD~~KI~~YNPLEQCCYND~~A~~IVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFVVKLKVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTGCCATT
TTCTGCATCTCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT
GCTATGATGATGCCGTGCGTGCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA
CTCAGCCGGACCTCGGATGACAGGCTTGTGCAGTGTCATAATGGAACATCAGGGAA
CGATGACTCCTGGATTCTCCTCCTGGGTGGGCCTGGAGAAAGAGGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTGGGGCCAGAGAAACACACACTCAACTGCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT
GACCCCTATGCCAACATCAACCCGGCACCACCCAAGGCTGGCTGGGAACCCTCACCCCT
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLCSHGAPVAPMTPYLMCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGCCGCCCCGAGCGCTCACTCGCTCGCACTCAG
TCGCAGGGAGGCTCCCCCGCCGGCGTCCCAGCCGCTCCCGGGCACCAAGAGTTCCCTCT
GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGAGCTGGCGCTGGGA
TCCCTGCTCTCGCTCTTCCCTGGCTCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTCGC
CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGCAGAACGTCACCCCTCACCTGCAGGCTCT
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTCTACAAGACGTGGTACCGCAGCTCGAGG
GGCGAGGTGCAGACCTGCTCAGAGGCCGGCCATCGCAACCTCACGTTCCAGGACCTTCA
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGGCCACGACCTGGCTCAGGCCACGGC
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGAACCTGACCCCTGCTG
GATAGCGGCCTACTGCTGCCTGGTGGAGATCAGGCACCACACTGGAGCACAGGGT
CCATGGTGCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACACTGTGTGGTGT
ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
ATCGTAGGAATCCTCTGCCTCCCCCATCCTGCTCCTGGCTACAAGCAAAGGCAGGCAGC
CTCCAACGCCGTGCCAGGAGCTGGTGCAGGATGGACAGCAACATTCAAGGGATTGAAAACC
CCGGCTTGAGCCTCACCACTGCCAGGGGATAACCGAGGCCAAAGTCAGGCACCCCCCTG
TCCTATGTGGCCAGCGGCAGCCTCTGAGTCTGGCGGCATCTGCTTCGGAGGCCAGCAC
CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTCCCACCCCTGGGACCCCTGACT
CTCCAAACTTGAGGTACATCTAGCCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGGCTGG
GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTGGCCTGGCCCTGGTTC
CCTCCCTCTGCTCTGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCTCAACCCCTC
TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTGGGCTGAG
ATTCTCCCTAGAGACCTGAAATTACCACTACAGATGCCAAATGACTTACATCTTAAGAA
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTGGGATGTGGCA
GCATCAGTGGACAAGATGGACACTGGCCACCCCTCCAGGCACCAGACACAGGGCACGGTG
GAGAGACTTCTCCCCGTGGCGCCTGGCTCCCCGTTTGGCCAGGGCTGCTCTGTC
AGACTTCTCTTGTACACAGTGGCTCTGGGCCAGGCCTGCCACTGGCCTGCC
ACCTTCCCCAGCTGCCTCTACCAGCAGTTCTGTAAAGATCTGTCAACAGGTTAAGTCAAT
CTGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTGGTGGTCCGAAACGGGAAGTAC
ATATTGGGCACTGGTGGCCTCCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG
ATGTTGCCCAACCACTGGAGATGGTGCTGAGGGAGGTGGTGGGCCCTCTGGGAAGGTGA
GTGGAGAGGGCACCTGCCCTCCCCATCCCTACTCCCACGTGCTCAGGCCAGGG
ATTGCAAGGGTGCACACAATGTCTGTCCACCCCTGGACACTTCTGAGTATGAAGCGGGAT
GCTATTAAAAACTACATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLEASAD
HHGNFSITMRNLTLLDGLYCCCLVVEIRHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPPGDVFFPSLDPPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTCTGCTGGACCTCCTCGTCTCCATCTCTCCCTCCT
 TTCCCCGCGTTCTCTTCCACCTTCTCTTCCCACCTAGACCTCCCTGCCCTCC
 TTTCTGCCACCACGCTGCTCCTGGCCCTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTCTCCCTCCCTCCGA
 CTCCGCTCCGGACCAGCGGCCTGACCTGGGAAAGG**ATG**GTTCCCGAGGTGAGGGTCCTC
 TCCTCCTGCTGGACTCGCGCTGCTGTTCCCCCTGGACTCCCACGCTCGAGCCGCC
 AGACATGTTCTGCCTTTCCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCATGTGAGT
 TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCTGTGACGGAGCCACAGCAATG
 CTGTCCAAGTGTGTAACCTCACACTCCCTCTGGACTCCGGCCCCACCAAAGTCCTGCC
 AGCACAAACGGGACCATGTACCAACACGGAGAGATCTCAGTGCCATGAGCTGTTCCCCCTCC
 CGCCTGCCAACCAACCAGTGTGCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCGAACCAACCAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGAGAAAGAGAGGGCCGGCACCCAGC
 CCCCACTGGCCTCAGGCCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACTGTCAAGATCGTCTGAAGGAGAACATAAGAAAGCCTGTGTCATGGGG
 AAGACGTACTCCCACGGGAGGTGTGGCACCCGCCCTCCGTGCCTCGGCCCTGCCCTG
 CATCCTATGCACCTGTGAGGATGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGGACAAA
 GCAGACCCCTGCCACAGTGAGATCAGTTCTACCAAGGTGTCCAAGGCACCGGGCGGGTCCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTGCCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTTCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTCCAGAAAGAGGGCACAGCACTCCGACTGCTCGCTGCCAC
 GAAGGTCAGTGGAACGTCTCCTAGCCAGACCCCTGGAGCTGAAGGTACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACC**TAA**CAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAATAAGAAGTGCATTACCTCAAAAAAAAAAAAAAAA

FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELPSPRLPNQCVLCSCTEGQIYCGLTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPGT PAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV
KDEETEAQRGEVPGPRPHSQNLPLSDQESQEARNPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGC GGCTGC GGGGAGCTCCC
GTGGGGCCTCCGCTGGCTGTGCAGGC GGCCATGGATT CTTGC GGAAAATGCTGATCTCAGT
CGCAATGCTGGCGCAGGGGCTGGCGTGGCTACGCGCTCCTCGTTATCGTGACCCGGAG
AGCGGCCGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAAGGAGCAGGGAGGAG
GC GGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAACTGGATGGTTGGCGCGAAGGC GGCGCCAGCGGGAGGTACCGT
GAGACCGGACTTGCCTCCGTGGCGCCGGACCTTGGCTGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTCGTGGCCCAGCGGAGAGTCGGACCGAGATAACCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGGGTGAGCACGTTCCCCAACCCCTGGACTGACTGCTTTAAGGT
CCGCAAGGC GGCCAGGGCCAGACGCGAGTCGGATGTGGTGAAGTGAACCAATAAAA
TCATGTTCTCCAAAAA
AAAAAAAAAAA
AAAAAAAAAAA

FIGURE 88

MDSLRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLA
TLQEAAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAAGCTAACCCCTGGGCTTGAGGGGAAGA
 GGCTGACTGTACGTTCTTCTACTCTGGCACCACTCTCCAGGCTGCC**TG**GGGCCAGCACC
 CCTCTCCTCATCTTGTTCCTTTGTATGGCGGGACCCCTCCAAGGACAGCAGCACCACCT
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGGCCAGTGCCAGGACC
 AGAGTAGTCGGCATGCTGCTGAGCTGCGGACTTCAAGAACAGATGCTGCCACTGCTGGAG
 GTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCACACCCTCCGGAGAGTGGA
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTGCGCCTGTGTAGAGT
 TTGATGAGAAGGTGACTGGAGGCCCTGGACCAAAGGAAGGAAGGAATGAGAAGTAC
 GATATGGTACAGACTGTGGCTACACAATCTCAAGTGAGATCAATGAAGATTCTGAAGCG
 ATTTGGTGGCCCAGCTGGCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACG
 TGTTAGATGGGACACAGAACATGACACAGCCTTGTCTTCCCAGGCTGCGTACTTCACCCTT
 GCCATGGCTGCCCGAAAGCTTCCCAGTCCGGTGCCTTCCCCTGGTAGGCACAGGGCA
 GCTGGTATATGGTGGCTTCTTATTTGCTCGGAGGCCTCTGGAAGACCTGGTGGAGGTG
 GTGAGATGGAGAACACTTGCAGCTAACAAATTCCACCTGGCAAACCGAACAGTGGTGGAC
 AGCTCAGTATTCCCAGCAGAGGGCTGATCCCCCTACGGCTTGACAGCAGACACCTACAT
 CGACCTGGTAGCTGATGAGGAAGGTCTTGGCTGTCTATGCCACCCGGGAGGATGACAGGC
 ACTTGTGTCTGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCA
 TGTCCCAGAGAGAACATGCTGAGGCTGCCTTGTATCTGTTGACGCCAGCGGACCCCTGACCC
 CACCCGTCCTGCCAGTCGGGCCGCATCCAGTGCTCCTTGATGCCAGCGGACCCCTGACCC
 CTGAACGGGCAGCACTCCCTATTTCCCCCAGATATGGTGCCTATGCCAGCCTCGCTAT
 AACCCCCGAGAACGCCAGCTATGCCCTGGATGATGGCTACCAGATTGTCTATAAGCTGGA
 GATGAGGAAGAAAGAGGGAGGAGTT**TG**AGGAGCTAGCCTGTTGCATCTTCTCACTC
 CCATACATTATATTATATCCCCACTAAATTCTTGTCTCATTCTCAAATGTGGCCAG
 TTGTGGCTCAAATCCTCTATATTTAGCCAATGGCAATCAAATTCTCAGCTCCTTGT
 TCATACGGAACTCCAGATCCTGAGTAATCCTTGTAGGCCAGAGTCAAAACCTCAATG
 TTCCCTCCTGCTCTGCCCATGTCAACAAATTCAAGGCTAAGGATGCCAGACCCAGG
 GCTCTAACCTTGTATGCCAGGGCAGGCCAGGGAGCAGGCAGCAGTGTCTTCCCTCAGAGTG
 ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTGTCTCTCTTCCCTCACTCCTCCCT
 TCAGTGTCTGAGGAACAGGACTTCTCCACATTGTTGTATTGCAACATTGCAATTAAA
 AGGAAAATCCACAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSGPLQGQQHHLVEYMERRLAALERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRGFGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPR
RDFTLAMAARKASRVRFVFPWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTCCGCACCTGAGCATTAGGCCAGTTCTCCTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
 CTCTCATGCTCAGTTGGTCTGAGTCTCCTCAAGCTGGATCAGGGCAGTGGCAGGTGTT
 GGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAGGACGCAGCATTCTCCTGTTCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGGTTCTCAGGGCCAGTTCTAGCGTGG
 TCCACCTCTACAGGGACGGAAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAAAATGGTGAAGGATTCTATTGGGGCGCATCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTCCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGCTCAGTTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCAGTCCTCGGGCTGGTCCCCGGCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTGGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTCA
 GCCTATATCGTGGCACCTGGTACCAAAGTACTGGGAAATACTCTGCTGTGGCTATTTTG
 GCATTGTTGGACTGAAGATTTCTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTCCAAGCAGGGAAACATTACTGGAGGTGGACGGAGGACACAATAAGGTG
 GCGCGTGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTGTATTCACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGTCTCCTGGACTATGAGTG
 TGGGACCATCTCCTCTTCAACATAATGACCAAGTCCCTATTACCCCTGACATGTCGGT
 TTGAAGGCTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTGGCAAAGGGCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTCCTCCCCAGGG
 GTGAAATGTAGGGATGAATCACATCCCACATTCTCTTAGGGATATTAAGGTCTCTCCCA
 GATCCAAAGTCCCGAGCAGCCGCCAAGGTGGCTCCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGAGGAAGAAGGCTGACATTACATT
 AGTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGATCCTAATGGTTGTTCAATTATACACTTCAGTA
 AAAAAA

FIGURE 92

MALMLSVLSSLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQP FMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQK
AIWELQVSALGSVP LISITGYVDRDIQLLCQSSGWFPRTAKWKGPGQDLSTDRTNRDMH
GLFDVEISLTQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAE LDWRRKHGQAE LRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQE VPHESEKRFRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL
PDHG YWVLRLNGEHLYFTLNPRFISVF PRT PPTKIGVFLDYECGTISFFNINDQSLIYTLC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATT PFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCGGTGGCGGTGGCGCGGTTGCGGAGGCTTCCTGGTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGC
CATGAGGGAGCCTGCCGAGCCTGGCGGCCTGCCCTGTTGTGCTGCCGCCGCCGCC
 CCGTCGCCTCAGCCGCCCTCGGCGGGGAATGTCACCGGTGGCGCGGGGCCGCCGCC
 GACGCGTCGCCGGGCCCCGGTTGCGGGGCGAGCCCAGCCACCCCTCCCTAGGGCGACGG
 TCCCACGGCCCAGGCCCCGAGGACCGGGCCCCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTTTGGGCACTGCTGGACCCCTTCC
 ACCACCTTCAGGCGCCGCTGGCCCTCGCCGACCACCCCTCCGGCGCGGAACGCACTTC
 GACCACCTCTCAGGCGCCGACCAGACCCCGCGCCGACCACCCCTTCGACGACCAC
 CGCCGACCACCCCTGTAGCGACCACCGTACCGGCCACGACTCCCCGGACCCGACCC
 GATCTCCCAGCAGCAGCAACAGCAGCAGCTCTCCCCACCCCTGCCACCGAGGCCCC
 TTGCGCTCCTCCAGAGTATGTAACTGCTCTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACACAGGGCAGTGTGAGTGTGGCCAGGTTATCAGGGGCTCACTGTGAA
 TGCAAAGAGGGCTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGT
 ACATGGAGCTCTAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAACTGAAGTT
 ATTATTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTAAACAA
 GAGGATGAGGGTCATAGATTACAAAATATTATATACTTTTATTCTTACTTTATG
 TATATTAAATGTCAGGATTAAAAACATCTAATTACTGATTAGTTCTC
 AGTCGCAATTTCCTCTGGATAATTCTGTAAATTCTGGAAAAAAATTATTGAAGA
 AAATCTGCTTCTGGAGGGCTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTT
 ATGTTATTAATATACCATGGAGTTGAGGAATTGTTGTTGGTTATTTCTCT
 ATCAAAATTCTACATTGTTCTTGGACATCTAACGCTTAACCTGGGGTACCT
 TTAACTAGTGGTAAGTAGACTGGTTACTCTATTACAGTACATTGAGAC
 TAGATTAAAGCAGGAATTATCTTAAACTATTGTTATTGGAGGTAATT
 ATAATGTAAGTGTATCTAACGCTTGTACTGCACTGAAAGTAATT
 ATTCTGGACCT
 TATGTGAGGCACTGGCTTTGTGGACCCAAGTC
 AAAAAGTGAAGAGACAGTATTAAAT
 AATGAAAAAAATAATGACAGGTTACTCAGTGTAACTGGGTATAAC
 CCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTGGCAAGTAATT
 CCTTCACTGAGCTGTTCT
 GTTGTGAAGATTAAATGAGTTGATATATAAAATGCCTAGCACATGT
 CACTCAATAA
 TTCTGGTTGTTAATTCAAGGAATT
 ACTTTAGCTCCTGACAAAGAAGTGT
 TTTAATCTGACTGTTAATT
 TAAATGATATTATACTGTTATGGAATT
 AGGCTGGCGCGGTGGCT
 CACGCCGTAAATCCTAGCA
 CTTGGGAGGCCAAGGCGGGTGGAT
 CACTTGAGGCCAGGAGTT
 CAGTGTGAGCTGGCAG
 CAGTGTGAGCTGGAGGCT
 GAGGCAGGAGAATCGGTT
 GAACCCGGGAGGTGGAGGTT
 GCAGTGAGCTGAGATCGCGCC
 CA
 CACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCT
 AAAAAAAAAAAAAAAA
 A

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGALLCCAAAAAVASAASAGNVTGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTPPAAERTS
TTSQAPTRPAPTTLSTTGAPTPVATTVPAPTPRTPTDLPSSNSSVLPTPPATEAPS
SPPPEYVCNCVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGGAATGGGCGGCTGCTGCTGGCTGCTTTCTGGCTTG
TCTCGGTGCCAAGGCCAGGCCGTGTGGTGGAAAGACTGGACCCCTGAGCAGCTCTGGG
CCCTGGTACGTCTGGGTGGCTCCGGAAAAGGGCTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGTGGTGGTACCCCTCACTCCAGAAAACAACCTGCGGACGCTGCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTGAGAATCCCTCAATAGCGTGCTGGAGCTCTGGGTGCTGCCACCAACTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTCAGGAGCCATGGGCTTCAACACCAGTGAGCTGT
ACAGTCTGACGGAGACAGCCAGCAGGAGGCCATGGGCTTCAACACCAGTGAGCAGGAGC
CTGGGCTCCTGTCACAGTAGCAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGGCCACAGGGCTGTGACCTCGGCA
GTGTCCACCCACCTCGCTCAGCGCTCCGGGCCAGCACCAGCTCAGAATAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPEPNLRTLSSQHGLGGCDQSVMIDLIRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTTAACCCCAGAC**ATG**CTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTACCCCTCGCAT
 GGCTGGATTACCCCTGGCCCAGTAGTCATGGCTACTGGTCCGGAAAGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTGGCAGTGTGGAGGAGACTGGGACC
 GATTCCACCTCCTGGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGA
 AGAAGTGTGATGCAGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG
 GCACCCCTGGAGTCCGGCTGCCCGAGAACATGTGACCTGCTCTGTGCCCTGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACAC
 CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCAGGACCATGGCACCGCCTCACCTGTC
 AGGTGACCTTCCCTGGGCCAGCGTGACCACGAACAAGACCGTCCATCTAACGTGTCTAC
 CCGCCTCAGAACTTGACCATGACTGTCTCCAAGGGAGACGGCACAGTATCCACAGTCTGGG
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCTGTGCC
 TCACAGCCCTAAACCGGGGGTGTGGAGCTGCCTGGTGCACCTGAGGGATGCAGCTGA
 ATTACACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCC
 AGAGCAAAGCCACATCAGGAGTGAUTCAGGGGTGGTCGGGGAGCTGGAGCCACAGCC
 GTCTTCTGTCTCGTCATCTCGTTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGCATAGAGGATGCAAACGCTGTCAGGGGTTCA
 CTCAGGGGCCCTGACTGAACCTGGCAGAACAGACAGTCCCCCAGACCGCCTCCCCAGCT
 TCTGCCGCTCTCAGTGGGGAGAGGAGACTCCAGTATGCATCCCTCAGCTCCAGATGGT
 GAAGCCTTGGACTCGCGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGA**TGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTGTAGAATTAACAGCCCTAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAGAACACAGGCTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTATTTTTAACAAAAGACAGACAAATTCTA

FIGURE 98

MLLLLPLLGGRERAEGQTSKLLTMQSSVTVQEGLCVHVPSCFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVNTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMVFQGDG
TVSTVLNGSSLSLPEGQSLRLVCAVDADSNPPARLSLSWRGLTLCPSQPSNPVGLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSRPAAVGDTGIEDANAVRGSAQGPLTEPWAEDSPPDQPPPASARSSVGEHELQYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCAGTGACCTGCCGAGGTGGCAGCACAGAGCTGGAGATGAAGACCCTGTTCTGGTACGCTCGGCCTGGCGCTGCCCTGTCCTCACCCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCATAAGGACTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGCGGTGGAAAGTTGGAAGGCCACGTTCACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCAC
ACATCTTTACTGCAAAGACCAGCACCATGGGGCCTGCTCACATGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCAGGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTCACGCCCTGCAGACGGGAAGCTGCGTTCCGAACACTAGG
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCCTACCACCAAGACACAGAGGCCGGACCACCT
GGACCTACCCCTCCAGCCATGACCCCTCCCTGCTCCACCCACCTGACTCCAAATAAGTCCT
TTTCCCCAAA

FIGURE 100

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKILMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Important features:

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTCGAG
 TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCCGCTACTCTGTGG
 GGCGACGCTCATGCCCGAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACA
 TAGTTCACCTGGGCAGCACAACTCCAGAAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTCCCCCACCCGGCTCAACAACAGCCTCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACAGCTGCCTCATTCCGGCTGGGCAGCACGTCC
 AGCCCCCAGTTACGCCTGCCTCACACCTTGCATGCCAACATCACCATATTGAGCACCA
 GAAAGTGTGAGAACGCCAACCCGGAACATCACAGACACCATTGGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTACTCCGGGCCCTGGTCTGTAACCAGTCTCTT
 CAAGGCATTATCTCCTGGGCCAGGATCCGTGTGCGATCACCGAAAGCCTGGTCTACAC
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAA**TAG**ACTGGACCCA
 CCCACCACAGCCATCACCCCTCATTCCACTTGGTGTGGCTCTGTTCACTCTGTTAAT
 AAGAAACCTAACCAAGACCCCTACGAACATTCTTGGCCTCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTCTGTTGATCCCCAGCCCCA
 AAGACAGCTCTGCCATATATCAAGGTTCAATAAATATTGCTAAATGAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISWGGSTSSPQLRLPHTLRCANITIIIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDGGPLVCNQLQGIISWGQDPCAIRKPGVYTKVCKYVDWIQETMKNN
```

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTGCTGGAGCCG**ATG**CCAAAACCATGCATTCTTATTCA
GAGATTGCTTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTTGATCGTCCAGAAAAGCTCTAACAGACAAGCA
AGAAGGGAGACCTACTAAATGCCATTATGACGGCTACCTGGCTAA
AGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTGTTGGTGGCAAGTCATA
AAAGGCCTAGACATTGCTATGACAGATATGTGCCCTGGAGAAAAGC
GAAAGTAGTATACCCCTTCATTGCTACATTGATTTGAGATTGAA
CTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTAA
ACAAATAGACATGGACAATGACAGGCAGCTCTAAAGCCGAGATA
AAACCTCTACTTGCAAAGGGAATTGAAAAGATGAGATATT
TTAAGAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAG
TTTAGAAGATATTGATTTGAAATGACCATGATGGTATGGCTTC
ATTCTCCAAGGAATACAATGTATAACCAACACGAT
GAACTA**TAG**CATATTGTATTCTACTTTTTTTAGCTATT
ACTGTACTTTATGTATAAACAAAGTCACCTTCTCCAAGTGTATT
GCTATTGCTATTCCCCTATGAGAAGATATTGATA
TCTCCCCAATACATTGATTTGGTATAATAAATGTGAGGCT
GTTTGCAAACTTAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL
```

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAA**ATG**CAGGGACCATTGCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTGGAGCT
GTGACTCAGAAAACCAAAACTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCAGTTCTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCC GTCTACTAAAATACAAAATCAGCCGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTGAACTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTAAAAAGAAAAGA
TAGTTCTTGTTCATTCGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSR

Signal peptide:

amino acids 1-18

FIGURE 107

CAAGCAGGTATCCCCTGGTGACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGCAC
 AGGGAAAGGGTACCTCTGAGATTCCCCTTTCCCCCAGACTTGAAGTGACCCACCATGG
 GGCTCAGCATTTTGCCTGTGTCTTGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTGAGGGCAC
 CAGCCTGCGCTGCGGGTGTCCTATTGACCACAGGTGGTCCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGAAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGTTCTGTGACCCATCCGGTACCTGGGAGCCTGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCCCTGCCGTCCCGTAACCAGCAGCGTTAAC
 CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGG
 ATCACCAACCACCCACGGAACCCATTCCGGATCTGCTCCAGTGCCTAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTATCCGGAGAACATCAGAGAACATGGTGTGAG
 GCGGCGTCCGGGCAGGATGCCAGGGTATTCTGGGGCCCTGGTGTGGGG
 GTCTCAAGGTCTGGTGCCTGGGGTCTGTGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGAACTGAC
 CTGTTCCCTCCACCTCCACCCCCACCCCTTAACCTGGTACCCCTGCCCTCAGAGCACC
 AATATCTCCTCCATCACTCCCTAGCTCCACTCTTGTGGCCTGGAACTTCTGGAACTT
 TAACTCCTGCCAGCCCTCTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAAATATAATGAAGGAGGGCAAAAAAA

FIGURE 108

MGLSIFLLLKVGLSQATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDGGPLVCGGVLQGLVSWGSVGPQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GC GGCCACACG CAGCTAGCCGGAGCCC GGACCAGGC GCGCTGTGCCTCCTCGTCCCTCGC
 CGCGTCCCGCGAAGCCTGGAGGCCGGAGCCCCCGCGCTGCC **ATG**TGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAAGGC GTTCGGCTTGCTCAAAGCCC GG CAGGAGAGGAGGCTGCC
 GAGATCAACCGGGAGTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTCCAGAAAA
 GCTCACAGCCTCAAAGAGAAGTACATGGAGTTGACCTGAACAATGAAGGC GAGATTGACC
 TGATGTCTTAAAGAGGATGATGGAGAAGCTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGTCAGTGACACTATACCTACCGAGACTTGAA
 CATGATGCTGGGGAAACGGTCGGCTGTCAAGTTAGTCATGATGTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCC **TGA**
 GGACCCCGCCTGGACTCCCCAGCCTCCCACCCATACCTCCCTCCGATCTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCATTTGTTGGTCATTGAGGGTTGTTGTGTT
 TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTAAAGGGCTCTGGTCGGGAATCC
 TGAGCCTGGTCCCCTCCCTCTCTTCCCTCCCTCCGCTCCGTGCAAGAGGCTG
 ATATCAAACCAAAACTAGAGGGGCAGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTCTTCGGTTCTGGACAGTGCCATGGTCCAGTGCTCTGGTGTCAACC
 AGGACACAGCCACTCGGGCCCCGCTGCCAGCTGATCCCCACTCATTCCACACCTTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAGGAGCTTGGCATTGGAGCCCTCAAGAAGG
 TACCAAGGAAGGAACCCCTCCAGTCCTGCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCA GCCCTACTGTCCCTTA CTGGGCAGCAGAGGGCTTGGAGGCAGAAGTGAGGCCTG
 GGGTTGGGGGAAAGGTCA GCTCAGTGCTGTTCCACCTTTAGGGAGGATACTGAGGGAC
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCAGTGGTAAGCCAAGA
 CTGAGAAAATACAAGGTTGCTTGTGACCCCAATCTGCTTGAAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMMLGKRSAVLKLVM
MFEGKANESSPKPVGPPPEDIASLP

FIGURE 111A

CGCGCTCCCCGCGCCCTCCTGGGCTCCACGCGTCTTGCCCCGAGAGGCAGGCCCTCCA
 GGAGCGGGGCCCTGCACACC**ATGCCCCCGGGTGGCAGGGT**C GGCGCCGTGCGGCC
 CGCCTGGCGCTGGCCTGGCGCTGGCAGCGTCTGAGTGGCCTCCAGCGTCGCCTGCC
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGCCTCCGCGGGTTC
 CTCGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATACCAAGGATC
 ACCAAGATGGACTTCGCTGGCTCAAGAACCTCCGAGTCTTGCATCTGGAAGACAACCAGGT
 CAGCGTCATCGAGAGAGGGCCTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
 AGAATAAGCTGCAAGTCCTCCAGAATTGCTTTCCAGAGCACGCCAGCTCACCAAGACTA
 GATTGAGTGAAAACCAGATCCAGGGATCCGAGGAAGGCCTCGCGGCATACCGATGT
 GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTCCGAGCGC
 TGCAGATTGGAGATCCTTACCTCAACAAACAACATCAGTCGCATCCTGGTCACCAGC
 TTCAACCACATGCCAAGATCCGAACTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
 CCACCTGGCCTGGCTCTGGATTGGCTGCCACAGCGACGGACAGTTGCCAGTTCAACTCT
 GCATGGCTCCTGTGCATTGAGGGCTTCAACGTGGCGATGTGCAGAAGAAGGAGTACGTG
 TGCCCAGCCCCACTCGGAGCCCCATCTGCAATGCCAACTCCATCTCCTGCCCTCGCC
 CTGCACGTGCAGCAATAACATCGTGGACTGTCGAGGAAAGGGCTTGATGGAGATTCTGCCA
 ACTTGCCGGAGGGCATCGCAAATACGCCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA
 GGAGCCTTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TATTGCTCCAGATGCCTCCAGGGCTGAAATCACTCACATCGCTGGCCTGTATGGGAACA
 AGATCACCAGAGATTGCCAAGGGACTGTTGATGGGCTGGTGTCCCTACAGCTGCTCCCTC
 AATGCCAACAAAGATCAACTGCCCTGGGTGAACACGTTTAGGACCTGCAAGAACCTCAACTT
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGCTTCTGCCCTCTGCAGT
 CCATCCAGACACTCCACTTAGCCAAAACCCATTGTGTGCAGTGCCTGAAGTGGCTG
 GCCGACTACCTCCAGGACAACCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCGGCCG
 ACTGCCAACAGCGCATGCCAGATCAAGAGCAAGAACGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTCAGCAGCGAGTGCTCATGGACCTCGTGTGCCCTGAGAAGTGTG
 TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGGCCACCTCCC
 TGAATATGTCAACGACCTGCACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCAACCTGCGGAAAATAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT
 GGAGACCGTGCACGGCGCGTGTCCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA
 GTAACCTGATCAGCTGTGAGTAATGACACCTTGCCGGCTGAGTTGGTGTGAGACTGCTG
 TCCCTCTATGACAATCGGATCACCACCATCCCCCTGGGGCCTTCACCACGCTGTCTCCCT
 GTCCACCATAAACCTCTGTCCAACCCCTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
 AGTGGTGAGGAAGAGGCGGATGTCAGTGGAACCCCTAGGTGCCAGAACGCCATTTCCCTC
 AAGGAGATTCCCACCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCCGCGTGCCCGGAGCAGTGCACCTGTGATGGAGACAGTGGTGC
 GCAGCAACAAGGGCTCCGCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC
 CTGGAAGGAAACCACCTAACAGCGTGCCTGCCAGAGAGACTGTCGGCCCTCCGACACCTGACGCT
 TATTGACCTGAGCAACACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
 ACCTCTCCACTCTGATCCTGAGCTACAACCGCTGAGGTGCATCCCCGTCACGCCCTCAAC
 GGGCTGCCGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTCCAGCGTTCTGAAGG
 CTCCTCAACGACCTCACATCTTCCCACATCTGGCGCTGGGAACCAACCCACTCCACTGTG
 ACTGCAGTCTCGGTGGCTGCGAGTGGGTGAAGGGGGGTACAAGGAGGCCTGGCATGCC
 CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCTGCTCACCAACCCCAACCCACCGCTT
 CCAGTGCAGAAGGCCAGTGGACATCAACATTGTGGCAAATGCAATGCTGCCCTCCAGCC
 CGTGCAGAATAACGGGACATGCACCCAGGACCCCTGTGGAGCTGTACCGCTGTGCCCTGCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGTTCAGCTGCTCCTGCCCTC
 TGGGCTTGAGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACACTACGTGTATCTGTCGCCACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCCTGTGTGCCCTGAGCTGAACCTCTGTCAGCATG
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTCACTGCGAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGCCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCTCAGGGCTTCAGTGGACCCCTGTG
 AACACCCCCCACCCATGGCCTACTGCAGACCCAGGCCATGCGACCACTGAGTGCCAGAAC
 GGGGCCAGTGCATCGTGGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTCGCCGG
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGCAAAGACTCCTACGTGGAACCTGG
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGCCACTGACAAGGACAAC
 GGCATCCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCGAGGCCACGT
 GCAGCTGGTCTATGACAGCCTGAGTTCCCCCTCAACACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGCAGTTACAGTGTGGAGCTGGTGACGCTAAACCAAGACCCCTGAACCTAGTAGTG
 GACAAAGGAACCTCAAAGAGCCTGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
 CCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCTTGCGCCAGGGCACGG
 ACCGGCCTCTAGGCCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
 GACTTCAAGGCCCTCCACCACAGTCCCTGGGGGTGTCAACCAGGCTGCAAGTCTGCAACCGT
 GTGCAAGCACGGCCTGTGCCGCTCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
 GCTGGACGGCCCACTCTGCACCAAGGGAGCCCTACTGCCCTGTGCCAGGCCACAGATGCCAC
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAAATGACTCTGCCATGCCCTGCTCAGCCTCAAGTGTCAACCATG
 GGCAGTGCCACATCTCAGACCAAGGGAGCCCTACTGCCCTGTGCCAGGCCGGCTTAGCCGC
 GAGCACTGCCAACAAAGAGAATCCGTGCCTGGACAAGTAGTCCGAGAGGGTGTCCGCCGCCA
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGCT
 GTGGGCCCAAGTGTGCCAGCCCACCCGCAAGCGCGGAAATACGTCTCAGTGCACAG
 GACGGCTCCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
C_{TAA}GCCCTGCCCGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGACAGCC
 ATGTGGGACCCCTGGTATTGACATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA
 AGAGAATATTAAGTATATTGAAAATAACAAAAAATAGAACCTAAAAA
 AAAAAA

FIGURE 112

MAPGWAGVGA AVR LAL ALA SVL SGPP AVAC PTK CTCSA ASVD CHGL RAV PRGI PRN
 AER LD DRNN ITRIT KMD FAGL KNL RVL HLED NQSVI ERGAF QDL KQL ER LRL NKN KQL V
 PELL FQST PKL TRLD LSEN QI QGIP RKA FRG IT DVKN LQD NNHIS CIED GA FR AL RD LE IL
 TLNNN NIS RIL VTS FNHMP KIRTL RL HS NHLY CDCH LAWL SDW LR QRT VGQFT LCMAP VHL
 RGF NVAD VQ KKEY VCP APH SEPP SCN ANS IS CP SPCT CSNN IVDC RGK GLME IPAN LPEGIV
 EIR LEQ NSI KAIP AGA FTQ YKKL KR IDIS KNQ IS DIAP DAF QGL KSL TSL VLY GNKITEIAK
 GL FD GLV S LQ LLL NANK IN CL RVNT FQ DLQ NL LS LYDN K LQT IS KGL FAPI QSI QTL HL
 AQNP FVCD CHL KW LADYL QDN PIET SGAR CS PR RL ANK RIS QI KS KK FRC SG SEDY RS RFS
 SEC FM DLVC PEK CRCE GTIV DC SNQ KLV RI PSHL PEY VT DLR LND NEV SV LEAT G IF KK LPN
 LR KIN L SNN KIKE VREG AF DGA ASV QEL M LTGN QLE TV HGRV FRGL S GLKT LM RSN L I SCV
 SNDT FAGL SS VR LL SLYDN RITT IT PG AFTT LV SL STIN LL S NP FNC NC HLA WL GK WLR KRR
 IVSGN PRC QK PFFL KEI PI QDV AI QDF TCD GNE ESS CQL S PRC PEQ CT CMET VVR CSN KGL R
 AL PRG MPK DV TELY LEGN HTA VPRE LSA RL HTL IDLS NN SIS MLT NYT FS NM SHL ST LIL
 SYNR LRC I PVH AFN GLR SLRV LTL HGNDI SS VPEG SFND LTSL SHL AL GTN PLH CDSL RWL
 SEWVK AGY KEP GIAR CS S PEP MAD RLL TT PTH RF QCK GPV DIN IVA KCNA CLS S PCK NNGT
 CTQDP VELY RC AC PYS YKG K DCT VP INT CI QN PCQ HGGT CHL SD SH KDG FSC S C PLG FEG QR
 CEIN PDD CED ND CENN AT CVD GIN NY VCIC PP NY TGEL CDE VID HC VP EL NLC QHE AKCI PL
 DK GF S CEC VPG YSG KLC ET DN DDC VAH KCR HGA QC VDT ING YT CT CP QGF SGPF CEH PPP MV
 LL QTSP CDQ YEC QNG AQC I VV QQE PTC RCP PGF AG PR CE KL IT VN FVG KDS YVEL ASAK VRP
 QAN ISL QV AT DK DNG ILL YKG DNDPL ALE L YQ GHV RL VY DS LSS PPTV YSV ET VND QF HS
 VEL VTL NQ TLN L VVD KGTP KSL GKL QK QPAVG IN S PLY LGG IPT ST GLS AL RQ GTDR PL GG F
 HGC IHE VRIN NEL QDF KAL PP QSL GV SP GCK S CT VCK HGL CRS VE KDS V CE CR PG WT GPL C
 DQE ARD PCL GH RCH HGK CV AT GT SYM CK CAEG YGG DL CDN KND SAN ACS AF KCH HGQ CH ISD
 QGE PY CLC QPG FGS GE HC QQ EN PCL GQ VV RE VIR RQ KG YAS CAT ASK VPI ME CR GG CGP QCC Q
 PTR SK RR KYV FQ CT DG SS F VEEVER HLE CCG CLAC S

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCA
GAECTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTCAGTTCTGTCT
CCGGCAGGCTTGAGGATGAAGGCTGCAGGCATTCTGACCCCTCATGGCTGCCTGGTCACAG
GCGCCGAGTCCAAATCTACACTCGTTGCAAACGGCAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGCCTGGATGACGGCAGCAGCATCGACTATGGCATCTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGAAAGCTGAAGGAGAACAAACACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTCCTAAACTGGAACTGGACCCAGGATGCTTGAGCAAC
GCCCTAGGATTGCAGTGAATGTCCAAATGCCTGTGTCATCTGTCCCCTTCCTCCAATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTAAGAAAATAAATATTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLLIGCLVTGAESKIIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSLITDDLTDAAIICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTGCATCCCACTGTCCTGTGTCGGAGGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCTATTAAAACCTGTACATGGCTCCC
 CATTGGTTTTGGAGAAAAGTTCAAGCTTTACCTGGTGTCTGCCTGTATCCCAGTGTT
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACTCCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTCTAAACGACTATAACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTAGTCAACAGCCAGTTCACAGCTGCTGTTAAGGAA
 ACATTCAAGTCCTGTCTCACATAGACCTGATGTCCTCATCCATCTCAAATGTCACCAAG
 CTTTGACTCAGTTGTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTGGCAGTGGAAAGCCCTAGTA
 CAGCTGCGTGGAAAGATTGACATCCAAGATTGGGAGAGGGTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTGGCCAGTATGTGACCTTCTGAGGTCTTCAGACAAACAGAAAATCTCC
 CTCCTCCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCACTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCCAGTCATTGCTGTTAATTGGGTGGACCCCTGGAGT
 CCATTGACCACAGTGTACAGGGTTCTGTGAGCCTGACCCGGTGCACCTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTCCTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTATAATCAGATTGTTTAAGATCTCCATTAATGTCATTGATTGATTGTAGACC
 CAGTTGAAACCAAAAAAGAACCTAGAATCTAACATGCAAGAGAGATCTTAAAGGAA
 CTTGAGTCTGAATGTGAGCCACTTCCTATATACACACCCCTGTCCACTTTCAGAAA
 AACCATGTCTTTATGCTATAATCATTCAAATTGGCAGTGTAAAGTTACAAATGTGGTG
 TCATTCCATGTTCACTGAGTATTAAATTATATTCTGGGATTATTGCTCTGTCTA
 TAAATTGAAATGATACTGTGCCTAATTGGTTTCAAGTTAAGTGTGTATCATTATCAA
 AGTTGATTAATTGGCTCATAGTATAATGAGAGCAGGGCTATTGAGTCCCAGATTCAAT
 CCACCGAAGTGGCACTGTCATCTGTTAGGAAATTGGTGTCTGTCTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTGTTAAGATAATTGTATTGCAACTGAGATATAA
 TAAAAGGTGTTATCATAAAAAAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEFKLFTLVSACIPVFRLARRKKILFYCHFPDLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAASFKETFKSLSHIDPDVLPSLNVTSDSVVPEKLD
DLVPKGKKFLLSINRYERKKNLTLALEALVQLRGRLLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

Ala Arg Lys Glu Asp Asn Gln Ser Thr Val Ile Leu Pro

FIGURE 117

400 350 300 250 200 150 100

GAATACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACGTAAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAAGTTGCATGAGTTCTGGTTAATTGCATGAGAGATATGGGCCTGTGGT
 CTCCTCTGGTTGGCAGGCGCCTCGTGGTAGTTGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCAATAAGACATCGGACCCCTTGAAACCAGTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACCTTGCCCTCCTCAAAGCTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTGGTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAACATGGCACAGTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGTCAC
 TTGATAAAAACATGACTCGGAAAAAACAAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGTCCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTCGAACTGCCA
 AACTGACTCCAGTTCTGCCAGCTTCAAGATATTGAAGGAAAATTGACCGATTATTATT
 CCTAGAGAGACCCCTGTCCTTATGCCCTGGTGTGGTACTTCAGGATCCTAATACTGGCC
 ATCTCCACACAAGTTGATCCAGATCGGTTGATGATGAATTAGTAATGAAAACCTTTCT
 CACTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTACCA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 ATTAAAAATTATACATTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTAAAAAA
 AAATCTATGTTGAATCCTTTATAAACCAGTATCACTTGTAAATATAAACACCTATTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGIPTEEKDGPNLPDIVNSGSLHEFLVN LH
ERYGPVVSFWFGRRLVSVSLGTVDVLKQHINPNKTSDPFETMLKSLLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLKDWL SYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQE VIRFQKNHGTVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDMSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFD PDRFDELVMKTFSSLGFSGTQECPELRFAYMVT TVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTGTCGGCTTGCAGGGAGACTCAGGAGTCGCTGTCTGAACCTCCAGCCTCAGA
GACC GCCGCCCTGTCCCCGAGGGCCATGGGCCGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCCAGGACAGCAACAT
ACAGGCCTGCCTGCCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATT CAGCTGG
TGGCCCGCTCTGTACCCCTGGGCCTTTGCAGTGGAGCTGGCCGGTTCCCTCTCAGGA
GTCTCCATGTTAACAGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTCTTCATATTGAGCGTTGGAGTGCACTA CGTATTGGTACATTTTGCT
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTATTGTCACCGTCTTGGCTGAAA
AAGAAACCC TTTGATTACCTCATGACGGAACCTAACGGACGAAGCCTACAGGGCAAGGG
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGATTATCCGATTGTATTAA
GTGCTTGTAATAAAATATGTTTAGTAACATTAAGACTTATACAGTTAGGGACA
ATTAAAAAAA

FIGURE 120

MGRVSLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCCGACCCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTGCCTGGCTCTCC
CCAGCCTCCTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCAGCTGGCTAC
AACTTCCTGATTGGAGAACGAGCAGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC
CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTCATGGCAACTACATGG
ATCAGGGTGCCACACCCAGGCCATCCGGCAGCCCAGGGTCTACTGGCCTGCAGGTGGCT
CAGGGAGCCCTGAGGTCAAACATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTTACACCTCATCCAGAATTGCCACACTACCGCTCCCC**TGA**GGCC
CTGCTGATCCGCACCCATTCCCTCCCTCCATGGCAAAAACCCACTGTCTCCTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNPASCQQQARNVQHYHMKTGLGCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNPASCQQQARNVQHYHMKTGLGCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCCTCCGGCTCAGAGGACCTGAGCGTATGACCACGAGGGCCAGCCCCGGCC
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAACGTCAGGCTCCGCCATGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGCATTCTTGGCAGCCCCCAACGCC
 CGAACACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGCAGCTTCTAC
 TCCAACATCAAGACGGTGGCCCTAACCTGCTCACAGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCAAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTCCCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATTTCATCGAACGCCAAG
 GCCTCCAAAATCTCAACTGCCGGATGGAGTGGAGAAGGTAGAACGGGCCGGACCTC
 GCTTGACCCACGCCAGCCAAGATCTGCTCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGCCCTCAAAGTCGTCTGTCTACATGCCCTTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGTACCCCCCTACTACCCATC
 TGGG**TGA**CCCGGGGCAGGCCACAGAGGCCAGGGCTGGAAAGGACAGGCCCTGCCATGC
 AGGAGACCATCTGGACACCAGGGCAGGGAAAGGGTTGGCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCAAGTG
 CTGGTCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGTGGCT
 CTCTGTGCAGCCTCACAGGGCTTGCCACGGAGCCACAGAGAGATGCTGGTCCCCGAGGCC
 TGTGGCAGGCCGATCAGTGTGGCCCAGATCAAGTCATGGAGGAAGCTAACGCCCTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGTGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGCGCCCTGAGCCCTTGTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCTGGGTCTTGATGTCTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTCCAAAATTCCCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTAACGTAAGACAGGACGATTGTGGCCTCCCACACTAAGGCC
 ACAGCCCATCCCGTGTGTGTGTCCTCTCCACCCCAACCCCTGCTGGCCTCTGGAG
 CATCCATGTCCGGAGAGGGGTCCCTAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGTGGGGGGGGGGGGGGCAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTGTTGGGGAGGGGAGGGAAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTGTGTGAAGAATCGTGTCTGGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSILYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPLSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVCVDNYHSDTPY
YPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTGGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGAGACTTGACTTCAAGCCACAGAAT
 TGGTGGAAAGTGTGCGCGCCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGCACCAGGATCCCGGGTAGGAGGCACGCAGGGGAGCACCAGGCCAGCC
 GGCTGCGGCTGCCAACACGGCTCAC**AT**GGCTCCGGCGCCGGCGCTGTCCGGTGGCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGCTGCCGTCTGGCACAGAACGACACGGAGCC
 CATCGTGTGGAGGGCAAGTGTCTGGTGGTGCAGCTGAACCCGGCACGGACTCCAAGG
 GCTCCTCTCCTCCCCGCTGGGATATCGGTCCGGCGGCCACTCCAAGGTGCCCTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTACTT
 CGATCAGATCCTGGTGAATGTGGTAATTTTACATTGGAGTCTGTCTTGACCAAA
 GAAAAGGAATTACAGTTACAGTTACGTTACGTTACGTGATTAAAGTCTACCAAGGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTGCAGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTACCTAA
 AACTGGAGAAAGGTAAATTGGTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT
 TTCCCCCTA**TAG**GATTCAATTCTCCATGATGTTACCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTCATCATTGGATTGATGTTCTTATTGGTTCTCATGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTACAGATTATTGTG
 TGTGTCTGTTCAAGTATATTGGATTGGACTCTAACAGATAATACCTATGCTAAATGTA
 ACAGTCAAAAGCTGCTGCAAGACTTATTCTGAATTCTATTGGATTACTGAATTAGT
 TACAGATGTGGAATTTCATTGTTAGTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAAACTCTAAAGTCTGACTTCATCAACGGTTAGTGTGATACTGCCAAGAAACTGTATACTG
 TGTTAATATATTGATTATTTGTTTATTCTTGGATTAGTTGTTGGTCTGTAA
 AAAACTGGATTTCAGTAACGGTATTGTTCTCTAAAATAAGGTAAATGAA
 TGGCTTGCACAAATTACCTTGACTACGATATCATGACATGACTCTCTCAAAAAAAA
 GAATGCTTCAAGTGTATTGTTAAATTGTATATGTGAAAGAGTCATATTCCAAAGTTATT
 TTCTAAGAAGAAGAATAGATCATAAAACTGACAAGGAAAAGTTGCTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCGAGGGAAATCTTACCTTATTGC
 TCAACTTAATTAAAATGATTGATAATAACCACTTTATTAAAACCTAACGGTTTTTT
 TCCGTAGACATGACCACTTTATTAAACTGGTGGGGATGCTGTTCTAATTACCTAT
 TTTCAAGGCTCTGTTGATTGAAAGTATCATCTGGTTTGCCTTAACCTTTAAATTGTA
 TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTAGTGCATAT
 CTTGTCTTGTAGGTATATGAATTCAAAATTATTGTTAGTCTGTTAGAATAAAGA
 TTAATATATGTTAAAAAAA

FIGURE 126

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSPLGI
SVRAANSKVAFAVRSTNHEPSEMSNKTRIIYFDQILVNVNFGNFTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNMLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCCATGACTGC GGCCGTGTTCTCGGCTGCGCCTCATTGCCTCGGGCTGCGCTC
 GCCCTTATGTCTCACCATGCCATCGAGCCGTTGCGTATCATCTCCTCATGCCGGAGC
 TTTCTCTGGTGGTGTCTACTGATTCGTCCTGTTGGTCATGGCAAGAGTCATTA
 TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGTCTGTC
 TATATCCAAGAAATGTTCCGATTGCATATTATAAATCTTAAAAAAAGCCAGTGAAGGTTT
 GAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCGACTGCTGGCCTATGTTCTGGCT
 TGGGCTTGGAAATCATGAGTGGAGTATTCCTTGTAATACCCTATCTGACTCCTGGGG
 CCAGGCACAGTGGGCATTCATGGAGATTCCCTCAATTCTCCTTATTCAGCTTCATGAC
 GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA
 AAAAGTGGGCATCCTCCTATCGTTCTCCTGACCCACCTGCTGGTGTCA
 GCCCCAGACCTTC
 ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCA
 TGGGCAC
 CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
 ACAAGAACTTCTTACAACCAGCGCTCCAGATAACCTCAGGGAACCAAGCACTCCCAA
 ACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCCTTTCTGAAAATCCCTTTCTG
 GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

FIGURE 128

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP GTVGIGHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKW
GILLIVLLTHLLVSAQTFIISYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKN
FLLYNQRSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGC**A**TGTTGCTCTGGGCTGCCCTCT
 TGGTGCTCTTGGTGCCTCGGTGAGAGCCATCTGGGGTTCTGGGGCCAAGAACGTCAGCAAAGACGCCG
 AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCAGCTGGTCAACATCTACACCTCAACCATACTGTGACCC
 GCAACAGGACAGAGGGCGTGCCTGTCAGCAGCTGGTCAACATCTACACCTCAACCATACTGTGACCC
 TCCGCCAGAAGGAGGCTGTGGTCTCCAGGTGCCCTAATCTGCAAGGGATGTTTAGCGCAAGTACCTCT
 ACCAAAAAGTGGAACGAACCCGTGTCAGCCCCCACCAGAAATGAGTCGGAGATTCAAGTCTTACGTGGATG
 TGTCACCCGTGTCACCAGTCAACACCATACCAAGCTGGGTCAGCCGATGGACGATTTGTGCTCAGGACTG
 GGGAGCAGTTCAGCTCAATACCAACAGCAGCACAGCCCCAGTACTTCAGTATGAGTTCCCTGAAGGCGTGGACT
 CGGTAAATTGTCAGGTGACCTCAACAAGGCTTCCCTGTCAGTCATCTCCATTCAAGGATGTGCTGTCTG
 TCTATGACCTGGACAACAACGTAGCCTCATCGGATGTACAGACGATGACCAAGAAGGGCCATCACCGTAC
 AGCGCAAAGACTTCCCAGCAACAGTTATGTTGTTGGTGAAGACCGAAGACCAAGCTGCCGGGGCT
 CCCTGCCCTTCTACCCCTCGAGAAGATGAACCGGTCGATCAAGGGCACGCCAGAAAACCTGTCAGTGTGG
 TGTCTCAAGCAGTCAGTCTGAGGCATACGTCACTGGGATGCTTTGCTGGGATATTCTCTCCTTTAC
 TGCTGACCGTCCTCTGGCTGGGAGAAGTGGAGGCAGAAGAAGACCCGCTGGTGGCCATTGACCGAG
 CCTGCCAGAAGCGGTACCCCTGAGCTGGCTGATTCTTCTGGCAGTCCCTTATGAGGGTTACA
 ATGGCTCTTCTGAGAATGTTCTGGATCTACCGATGGTCTGGTGAACAGCGCTGGCACTGGGACCTCTTAC
 GTTACCAAGGGCCGCTCTTGAAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
 ACTACGACACATTGACCGACATCGATCCGACAAGAATGTCATCGCACCAAGCAATACCTCTATGTGGCTGACC
 TGGCACCGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAAGCAGTCACTCTGGAACATTGCCACATTGCTGTCT
 TCTATGCCCTTCTGTTGTCAGCTGTGATCACCTAACGACAGGGTGTGAATGTCACAGGAATCAGGACATCT
 GCTACTACAACCTCTGCGCCACCCACTGGCAATCTCAGCGCTTCACAACACCTCTCAGCAACCTGGGGT
 ACATCCTGCTGGGGTGTCTTCTGTCATCATCTGCAACGGAGATCAACCACAAACGGGCCCTGCTGCCA
 ATGACCTCTGTGCCCTGGAATGTTGGGATCCCCAAACACTTTGGCTTTCTACGCCATGGCACAGCCGTATGA
 TGGAGGGGTGCTCACTGCTTGTATCATGTGTGCCCAACTATACCAATTCCAGTTGACACATCGTTCATGT
 ACATGATCGCCGGACTCTGCATGCTGAAGCTCTACCAAGCGCACCCGGACATCAACGCCAGCGCTACAGTG
 CCTACGCCTGCCATTGTCATCTCTCTGTGCTGGGCTGGTCTTGGCAAAGGGAACACGGCGTCT
 GGATCGTCTCTCCATCATCAGCGCACCTGCTCCTCAGCACGAGCTCTATTACATGGGCCGGTGG
 AACTGGACTCGGGATCTTCCGCGCATCTCCACGTGCTCACACAGACTGCATCCGGCAGTGCAGCGGGCCG
 TCTACGTGGACCGCATGGTGCCTGGTCACTGGCAACGTCAACTGGTGCCTGGCTGCCATGGCTTATCA
 TGCGCCCAATGATTGCTTCTACTTGTGGCATTGGCATCTGCAACCTGCTCTTACTTGCCTTCTACA
 TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTGACCTCCGTGGTCT
 GGGGCTTCCGCTCTCTCTTCTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAAGAGTCGAGGGAGCACA
 ACCGGGACTGCATCTCTCGACTTCTTGAACGACCAAGCACATGGCACTTCTCTCCATGCCATGTTCG
 GGTCTTCTGGTGTGACACTGGATGACGACCTGGACTGTGAGCGGGACAAGATCTATGTTCT**CAGC**
 AGGAGCTGGGCCCTCGCTTACCTCAAGGGCCCTGAGCTCTTGTGTCATAGACGGGCACTCTGTCGTGCT
 GTGGGGATGAGTCCACGACCGCTGCCAGCACTGGATGGCAGGAGCAGCCAGGTCTAGCTTAGGCTTGGCCT
 GGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTCTGGCAGGGAGCAGGCCCTGCTCCCTGGAACCCCC
 AGATGTTGGCAAATTGCTGCTTCTCTCAGTGTGGGCTTCCATGGGCCCTGCTCTTGGCTCTCCATT
 GTCCTTGTCAAGAGGAAGGATGGAAGGGACACCCCTCCCATTCTCATGCCTGCAATTGCCCCCTCTCCTCCCC
 ACAATGCCCAAGCCTGGACCTAACGGCTCTTCTCCCATACTCCCACCTCAGGGCTAGTCTGGGGCTGA
 ATCTCTGTCTGTATCAGGGCCCCAGTTCTTGGCTGTCCTGGCTGCCATCACTGCCATCTCCAGTCAGCC
 AGGATGGATGGGGTATGAGATTGGGGTGGCAGCTGGTGCAGACTTTGGTGTAAAGGCCCTGCAAGGGG
 CCTGGGGCAGTGCCTTCTCTCCCTGACCTGTGCTCAGGCTGGCTTTAGCAATGCGCTCAGCCCAATT
 TGAGAACCGCCTCTGATTCAAGAGGCTGAATTCAAGAGGCTCACCTCTCATCCCATCAGCTCCAGTGTGCC
 AGCACCCAGGACTGGAGGGAGAACGCCCTACCCCTCCCTCTTCCAGGGCTTAGTCTTGCCAAACCCCC
 AGCTGGTGGCCATTGACACTGCCAAGAATGTCAGGGCAAGAGGAGGATGATAACAGAGTTCAG
 CCCGTTCTGCCCTCCAGCTGGGACCCAGTGCCTACCTTAAGAAAGGGCTTCAGGAAGGGATGTGCTGTT
 CCCTCTACGTGCCCTAGCTAGGCTCGCTTAGGACCCAGGGCTGGCTCTAAGTTCCGTCCAGTCTCAGGCA
 AGTTCTGTGTTAGTCATGCACACACATACCTATGAAACCTGGAGTTACAAAGAATTGCCCAAGCTCTGGG
 CCTGGCACCCCTGGCTTGGATCCCCCTGTCACCTGGTCAACCCAGATGCTGAGGATGGGGAGCTCAGG
 CGGGGCCCTCTGCTTGGGATGGAATGTTTCTCCAAACTTGTGTTTATAGCTGCTGCTGAAGGGCTGG
 AGATGAGGTGGGCTGGATCTTCTCAGAGCTCCATGCTATGGTGCATTCCGTTATGAATGAATT
 TGCAATTCAATAACCAACAGACTCAAAAAAAAAAA

FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLPKNVSQKDAEFERTYVDEVNSELVN IYTFNHTVTRNRT
EGVRVSVNVLNQKGAPLLFVVRQKEAVV SFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNNTYQLRVSRMDDFVLRTGEQFSNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFPCSVISIQDVLCPVYDLDNNVAFIGMYQTMTKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPV DQGHRQKTLSQLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPESGHPRVLADSFPGSSPYEGNYGSFENVSGSTDGL
VDSAGTGDL SYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLG YILLGLLFL LII LQREINHN RALLRN DLCAECGIPKHFG LFYAMGTALM
MEGLLSACYHVC PNYTNFQFDTSF MYMIAGLCMLK LYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTA FWIVFSIIHIIATLLLSTQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNL LLYFAFYIIMKLRSGERI
KLIPLL CIVCTS VVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCCTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCGCTGGAGGGCCTGTCTCG
ACCATGTCCCTGCCTGGCTGTGGCTGCTTGTCTCCGCCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCGTGGAAGTTCCAGAAAATATGGTGGAAATTCCCTTATACC
 TGACCAAGTTGCCGCTGCCCGTGAGGGGGCTGAAGGCCAGATCGTGTGTCAGGGACTCA
 GGCAAGGCAACTGAGGGCCCATTGCTATGGATCCAGATTCTGGCTTCTGCTGGTACCCAG
 GGCCTGGACCGAGAGGAGCAGGAGTACAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGTCACAGCCTGTGCTGTGACGTGAAGGATGAGAATGACCAGGTG
 CCCATTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACCAAGGCCTGGCATCCC
 CTTCTCTCCTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTGACCACGCCCTGGAGAGGAC
 CTACCAAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCCTATAACCGCACCATGGCCCAGGTACACTGGAGTGGGGTGTATGT
 GCACATCACCTGGAGAGCCATCCCCCGGACCCTTGAAGTGAATGCAGAGGGAAACCTCT
 ACGTGACCAAGAGAGCTGGACAGAGAACAGCCCAGGCTGAGTACCTGCTCAGGTGCGGGCTCAG
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGTGGATGAGAA
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCGGCTCCCCCAATTCC
 CACGTTGTATCAGCTCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGAGAGCCTTCCA
 GGTGGACCCCACCTCAGGCAGTGTGACGCTGGGGTGCTCCACTCCGAGCAGGCCAGAACAA
 TCCTGCTCTGGTCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTCAGCAGCACGTGT
 GAAGTCGAAGTCGAGTCAGATTAATGATCACGCCCTGAGTTCATCACTCCAGAT
 TGGCCCTATAAGCCTCCCTGAGGATGTGGAGCCGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCCTCCGCCTCATGGATTTGCCATTGAGAGGGAGACACA
 GAAGGGACTTTGGCCTGGATTGGAGCCAGACTCTGGCATGTTAGACTCAGACTCTGCAA
 AACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACGCCACGGTACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCCAAGTTGGACCAAGGAGAGCTACGAGGCCAGTGTCCCCATCAGGCC
 AGCCGGCTTTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCT
 CCCTAGTCATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGAGGTGCACACC
 GCCCAGTCCTGCAGGGCGCCAGCCTGGGACACCTACACGGTGCTTGTGGAGGCCAGGA
 TACAGCCCTGACTCTGCCCTGTGCCCTCCAATACCTCTGCACACCCGCCAAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGCCAGTGGCACGGTCCCTACAGC
 TTCACCCCTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC
 CCATGCCTACCTCACCTGGCCCTGCATTGGTGGAGCCACGTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTGAGTGATCGTGTGCGCTGCAAC
 GTGGAGGGCAGTCATGCGCAAGGTGGCCGATGAAGGGCATGCCACGAAGCTGTCGGC
 AGTGGGACATCCTGTAGGCACCCCTGGTAGCAATAGGAATCTTCTCATCCTCATTTCACCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCTGAAGGCG
 ACTGTC**TGA**ATGCCACGGCAGCTAGCTGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCAGCACCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT
 CTGCCCTGGGTGGAGGCACCATACCACCACTACCAGGCATGTCAGAGCCTGGACACCAAC
 TTTATGGACTGCCATGGAGTGCTCCAAATGTCAGGGTGGTGCCTGAAGAATAAAGCCCCA
 GAGAACTGGGCTGGCCCTATGGAAAAAAGAAAAAAGAAAAAAGAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAELYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRL
 GALALSPKGSTS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSIESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPPLELHVLVMMDENDNVICPPRDPVTASIPELSPPGTEVTRLSAEDADAPGSPNSH
 VVYQLLSPEPEDGVGRAFQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTE
 GTFGLDWEPDSGHVRLRLCKNLSYEAAAPSHEVVVVVQSVAKLVGPGPAGATATVTVLVERV
 MPPPQKLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSSEGWLCTIEKFSGEVHTA
 QSLQGAQPGDTYTVLVEAQDTALTTLAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRLQTLNGSHAYLTLLAHWVEPREHIIPVVVSHNAQMWMQLLVRVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTVAIGIFLILIFTHWMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

4 3 2 1 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

CCGGGGAC**ATG**AGGTGGATACTGTTCATTGGGCCCTTATTGGGTCCAGCATCTGTGGCAA
 GAAAAATTGGGGACCAAGTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTCTGGAAATCTCCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGCTCCATCTGTCAGTCTGCAGGCATTAAATCCTCCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTCAACTACGGG
 CTTACCATTCCCTGGAAGCTATTACACAGAGATGGACAAACATTGCCAGACTTCCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTGTTGAAAACCGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGGCCTGAGGCGCCGGCGTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACAGAGG
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTTCCTGTCCTGTCAGGCCAATCC
 TGATGGATATGTGTATACTCAAACCTAAAACCGATTATGGAGGAAGACGCCTCCGAAATC
 CTGGAAGCTCCTGCATTGGTGTGACCCAAATAGAAACTGGAACGCTAGTTGTCAGGAAAG
 GGAGCCAGCGACAACCCCTGCTCCGAAGTGTACCATGGACCCCACGCCAATTGGAAGTGG
 GGTGAAATCAGTGGTAGATTTCATCCAAAACATGGAATTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAGGCCAGATGCC
 GAGGAACCTGACAAGGTGGCGAGGCTTGCAGGCTAAGCTCTGGCTCTGTGTCGGGCACTGA
 GTACCAAGTGGTCCCACCTGCACCACTGTCTATCCAGCTAGCAGGAGCAGCATCGACTGG
 CGTATGACAACGGCATCAAATTGCATTACATTGAGTTGAGAGATACCGGGACCTATGGC
 TTCCTCCTGCCAGCTAACAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTAC**TAG**CGATGGCTCTGCTCTGTCTACATTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTTCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGTCCTGGGGTGTCCCTGCAAGAACCTGGTTCTGCCAGCCTGCTCAATTGGTCTG
 CTGTTTGATGAGCCTTGTCTGTTCTCCCTGCTGGCTGGCGGCTGCACTC
 AGCATCACCCCTCCTGGGTGGCATGTCTCTCTACCTCATTAGAACCAAAGAACATC
 TGAGATGATTCTTACCCCATCACATCTAGCCAAGCCAGTGACCTGCTCTGGTGGCACT
 GTGGGAGACACCACTGTCTTAGGTGGTCTCAAAGATGATGTAGAATTCTTAAATTTC
 TCGCAGTCTCCTGGAAAATATTCTTGTAGCAGCAAATCTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTGTTTTTTTTGAGACAGAGTTGCTCTGTTGCC
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTCACCAACCTCTGCCCTGGTTCAAGCA
 ATTCTCCTGCCTCAGCCTTGTGAGTAGCTGGTTATAGGCGATGCCACCATGCCCTGGCTA
 ATTTGTGTTTAGTAGAGACAGGGTTCTCCATGTTGGTCAGGCTGGCTCAAACCTCCA
 ACCTCAGGTGATGCCCTCTGGCCTCCAGAGTGTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCGTCCTTTAGGCCTGAATAACAAAGTAGAAGATCACTTCTTAC
 TGTGCTGAGAATTCTAGATACTACAGTTCTACTCCTCTTGTATTCACTGTG
 ACCAGGATGGCGGGAGGGATCTGTGTCAGTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTGCAGGATGGTAAATTATCCCCATCTGCTCTAAACTCAT
 CTTGCTCTTGAACTCACTCAAAGATCTAGGCCTCATCTTACAGGTCTAAACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCATTGCTGTGTGTGTGTT
 TCCTTGTCTGGTTGTGTGTGTGTGTGTGTGTGTTGTTGTTGTTGTT
 TCTGTCTATTGTATCCTGGACCACAAGTCCTAAGTAGAGCAAGAACATCAACCAGCT
 GCCTCTGTTTACCAACATGTGTAAATTCTAACCTCCTGCCTAGGATTGTACA
 GCATCTGGTGTGCTATAAGCCAATAATTCAATGTGAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDEMHQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAVWLNAAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRWNNASFAGKGASDNPCEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY
SQLLMYPYGVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAETWLGLKTIMEHVRDNLY

Signal peptide:

amino acids 1-16

FIGURE 135

FIGURE 136

MASLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDAVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT
KFTIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

GGCTGACCGTGTACATTGCCCTGGAGGAAGCCTAACCGAACCCAGGCATCCAGCTGCCAACGC
 CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG
 CCTTTATCTCTCACCTCAAGTCCCCTTCTCAAGAACATCCTCTGTTCTTGCCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTGCTTCCAGCCACAAAGAGACAGA**ATGAAGATGC**
 AGAAAGGAAATGTTCTCCTATGTTGGTCACTATTGCATTAGAAGCTGCAACAAATTCC
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCA
 GCGTGACCTCCAATGGGTCAGCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
 CTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGCCAGCACAGTCACCAACTCTGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGTGCACCAACTCTGA
 GTCTAGCACACTCTCAGTGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACCTCCA
 GTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCACAGCC
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACACTGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACAGCACCTCCAATGGG
 CTGGCACAGCCACCAACTCTGAGTCCAGCACAGCACCTCCAGTGGGCCAGCACAGCCACCAAC
 TCTGACTCCAGCACAGTGTCCAGTGGGCCAGCACACTGCCACCAACTCTGAGTCCAGCACGAC
 CTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCACCTCCAGTGGGCTAGCA
 CAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCGGCACAGCCACCAACTCTGAG
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCCAG
 TGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCA
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCACACTGCCACCAACTCTGAGTCCAGC
 ACAACCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGG
 TAGCACAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGAGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAAAC
 TCCAGTGGGCCAACACAGCCACCAACTCTGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACACAACCTCCATAGTCATCTACTGCAGTGAGTGAGGCAA
 AGCCTGGTGGTCCCTGGTGCCGTGGAAATCTTCCATCACCCCTGGTCTCGGTTGTGGCG
 GCCGTGGGCTCTTGCTGGCTCTCTCTGTGTGAGAAACAGCCTGCCCTGAGAAACAC
 CTTAACACAGCTGTCTACCACCCATGGCCTAACCATGGCCTTGGTCCAGGCCCTGGAG
 GGAATCATGGAGCCCCCAGGGCCAGGTGGAGTCCTAACCTGGTCTGGAGGAGACCAGTA
 TCATCGATGCCATGGAGATGAGCGGGAGGAACAGCGGCC**TGA**GCAGCCCCGGAAGCAAG
 TGCCGCATTCTCAGGAAGGAAGAGACCTGGCACCAAGACACTGGTTCCCTTCATTCATC
 CCAGGAGACCCCTCCAGCTTGTGAGATCCTGAAAATCTGAAGAAGGTATTCCCTCACC
 TTTCTGCCTTACAGACACTGGAAAGAGAACATCTATATTGCTCATTAGCTAACAAATAA
 ATACATCTCATCAACACACGACAAAGAGAACAGCTGTGCTGCCCCGGGTGGGTATCTAG
 CTCTGAGATGAACCTAGTTATAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA
 TCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 138

MKMQKGNVLLMFGLLLHLEATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSTSITSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSESSTTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNDSSTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTSSEASTATNSESSTVSSGISTVTNSESSTTSSGANTATNKGSSVTSGAGTAALTGMHTTSHSASTAVSEAKPGGSIVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGBHNHGAPHPRPRWSNWFWRRPVSSAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAAATAGCAGCGTGGCTCCCTGGCTCCTCTGCATCCTCCGACCTTC
 CCAGCAATATGCATCTTGCACGTCTGGTGGCTCCTGCTCCCTCCTGCTACTGGGGGCC
 CTGTCTGGATGGCGGCCAGCGATGACCCATTGAGAAGGTATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTGGAAATCACGC
 ATGCCGGAAGGAAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGAGGCCACACCGGC
 AAGGAGTTGGACAAAGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGAT
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCAGTGTGCTGGCCAGGCCGGGAAGGAGC
 TGCAGAATGCTCATATGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG
 GGCCTCAGTCAACACGCCCTTCATCAACCTCCGCCGTGGAGGAGCGTCGCCAACATCA
 TGCCCTAAACTGGCATCCGGCTTGCTGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
 ATGACCTGGAGGGTTGGGGTGGGGACAGGTTCTGAAATCCCTGAAGGGGTTGTACTG
 GGATTGTGAATAAACTTGATACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITAG
REVEKFVNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCGGGGTCCCCAGGGGCTGCCGCGGGCCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGG
CCC CGGGGGGCATGACCGTGCCTGACCTGACTCACTCCAGGTCCGGAGGCCGGGGCCGGGGCGACTCG
GGGGCGGACCGCAGGGCGAGCTGCCGCCGTGAGTCCGGCCAGGCCACCTGAGGCCAGGCCGGGGACACCGTC
GCTCCTGCTCTCCGAATGCTGCCAACCGGATGGGCTGAGGAGCTGGCTGCCGCCCATGGGCGCTGCC
CCTCGGGCACCGCTGCTGCTCCTGCTGCTGCTCCCTGCTGCCAGGCCGGCCCTCCGACCTGGGCGCTCAGC
CCCCGGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCCAGATTGAAGCTGAACACATCTCCAAC
ACAGCCCTCTGCTGAGCAGGGATGGCAGGACCTGTACGGGCTGCTGAGAGGCCCTTTGACTCAGTAGC
AACCTCAGCTTCCGCCAGGGGAGTACAGGAGCTGCTTGGGTGCAAGACGAGAAGAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGCAGTCAAAACATCAAGATCCTCCGCCGCTCAGCGGAGTCAC
CTGTTCACCTGTGGCACAGCAGCCTCAGCCCCATGTACATCAACATGGAGAACTCACCCTGGCAAGG
GACGAGAAGGGAAATGTCCTCTGGAAAGATGGCAAGGGCGTTGTCCTCGACCCGAATTCAAGTCCACTGCC
CTGGTGGTGTGATGGCGAGCTACACTGGAAACAGTCAGCAGCTCCAAAGGGAAATGACCCGGCATCTCGCGGAGC
CAAAGCCCTGCCGCCACCAAGGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTGTGGCCTCAGCCTAC
ATTCCCTGAGAGCCTGGCAGCTTGCAGGCGATGATGACAAGATCTACTTTTCTTCAGCGAGACTGGCAGGAA
TTTGAGTTCTTGGAAACACCATTGTGTCCTGCCGATTGCCGCACTGCAAGGGCGATGAGGGTGGAGAGCGGGGTG
CTACAGCAGCGCTGGACCTCCTCTCAAGGCCAGCTGCTGCTCACGCCGAGCATGGCTTCCCTTAAC
GTGTCAGGAGTCTTCAGCTGAGCCCCAGGCCAGACTGGCTGACACCCCTTCTATGGGTCTTCACT
TCCCAGTGGCACAGGGAACTACAGAAGGCTCTGCCGCTGTGCTTCACAATGAAGGATGTCAGAGACTTC
AGCGGCCTCTACAAGGAGGTGAAACCGTGGAGACACAGCAGTGGTACACCGTGACCCACCCGGTCCACACCCGG
CTGGAGCGTGCATACCAACAGTGCCCCGGAAAGGAAGATCAACTCATCCCTGCACTCCCAGACCGCGTGTG
AACTTCCCAAGGACCACTTCTGATGGACGGCAGGTCCGAAGCCGATGCTGCTGCAAGCCCCAGGCTCG
TACCAAGCGCTGGCTGTACACCCGCTCCGGCTGCAACCACACTACGATGTCCTCTGGCACTGGTAC
GGCCGGCTCCACAAGGCGAGTGGAGCGTGGGCCCCGGGTGACATCATTGAGGAGCTGCAAGATCTTCTCATGGG
CAGCCCGTGCAGAACTGCTCTGGACACCCACAGGGGGCTGCTGTATGCCCTCACACTGGGCTAGTCCAG
GTGCCATGGCAACTGCAAGCTGTACGGAGCTGTGGGACTGCCCTCGCCGGACCCCTACTGTGCTGG
AGCGGCTCCAGCTGCAAGCACGTCAGCCCTACAGCCTCAGCTGGCACAGGCCAGGGCTGGATCCAGGACATCGAG
GGAGCCAGCGCCAAGGACCTTGCAGCGCTCTCGGTTGTGTCCTCGTCTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTCCAGTCCAGGCCAACACAGTGAACACTTTGGCTGCCCTCCTCCAAACCTGGGACCCGA
CTCTGGCTACGCAACGGGGCCCCGTCAATGCCCTGCCCTCTGCCACGTGCTACCCACTGGGACCTGCTG
GTGGGCCCCAACAGCTGGGGAGTCCAGTGTGCTACTAGAGGAGGGCTCCAGCAGCTGGTAGCCAGCTAC
TGCCCAGAGGTGGAGGGAGCAGGGGGTGGCAGACCAAACAGATGAGGGTGGCAGTGTACCGCTATTATCAGCAC
TCGCGTGTGAGTGCACCGAGCTGGCAGGCCAGCTGGGTGAGCAGACAGGCTCTACTGAAAGGATCTGGTGTG
ATGTGCAAGCTTTGTGCTGCCGTGCTCTCCAGTTTATTCTTGCTCTACCGGACCCGAACAGCATGAAA
GTCTTCTGAAAGCAGGGGGAAATGTGCCAGCGTGCACCCAAAGACCTGCCCTGTGGTGTGCCCTGAGACCCCG
CCACTCAACGGCTAGGGCCCCCTAGCACCCGCTCGATACCGAGGGTACCGACTCCCTGTCAGACAGCCCCCG
GGGGCCCCAGTCTTCACTGAGTCAGAGAAAGAGGCCACTCAGCATCCAAGACAGCTCGTGGAGGTATCCCCAGTG
TGCCCCGGCCCCGGTCCGCCCTGGCTCGGAGATCCGTACTGTGGTTGAGAGCTGACTTCAGAGGACGC
TGCCCTGGCTCAGGGCTGTGAATGCTGGAGAGGGTCAACTGGACCTCCCTCGCTGCTCTCGTGGAAAC
ACGACCGTGGTGCCGCCCTGGAGGCCAGCTGGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
TACCAACAGACACCAACAGCCGCTGGCCCCAGAGGTCTGCCAAATATGGGGCTGCCAGTGTGGTGGAA
CAGTGTCTCTTATGAAACTGAGCCCTTGTGTTAAAAAAACATCCAAATGTGAAACTAGAATGAGAGGGAAAGAG
ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTGACATGGCTCCAGGGGTGCTGGGATGCATCCAAAGTGG
TTGCTGAGACAGAGTGGAAACCCCTCACCAACTGGCTCTCACCTCCACATTATCCGCTGCCACCGGCTGC
CCTGCTCTCACTGCAAGATTAGGACAGCTGGCTGCTGCTGCTGCTGCCAGTGCAGCCGAGGATGTAGTTG
TTGCTGCCGTGCTCCACCCACCTCAGGGACAGAGGGCTAGGTTGGCACTGCCCTCACCGAGGTCTGGGCTC
GGACCCAACCTCTGGACCTTCCAGGCTGATCAGGGCTGCCCCACAGCAGAGGGACAGCGCAGGCTCAGGAGAGA
TTCTGTCAGAACATGACCTTCCCTCAGGAAATTAGGAAAGAGAGTGTGCCCTGCCCTCGTGTGCGTGA
GAACCCGTGTGCCCTTCCCACCATATCCACCCCTGCTCCATCTTGAAACTCAAACAGGAGAAACTAACACTGCACC
CTGGTCCCTCTCCCCAGTCCCCAGTTACCCCTCACCTCCACTCTAACGGGATATCAACACTGCC
AGCACAGGGCCCTGAAATTATGTTTATACATTTTAATAAGATGCACTTTATGTCATTTTAATAAA
GTCTGAAGAATTACTGTTAAAAAAAAAA

FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPLL LLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDPAISRSQSLRPTKTESSLNWLDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARIICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRTTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYT VTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPG LHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP
QLATRPWIQDIEGASA KDLCSASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATR
LWLRNGAPVN ASASCHV LPTGDLLL VGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPIIISTSRV SAPAGG KASWGADRSY WKEFLVMCTLFVLAVLLPVLFL YRHRNSM
KVFLKQGECASVHPKT CPVVL PPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFT ESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCCGCCGCCGCCGCGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA
 GCCCAGCCAGCCGGAGGACGCCGCCAGGGCGGGACGGGAGCCCCGACTCGTCTGCCGCCGCCGTGCGCGTCG
 TGCCGGCCCCCGCTCCCCCGCGCGAGCGGGAGGAGCCGCCACCTCGCCGCCAGGCCGCCGTAGCGCCGCC
 CGGGCATGGTCCCCCTCTAAAGGCGCAGGCCGCCGGGGGGGGGGACTCGTCTGCCGCCGCCAGGCCGCCGTAGCGCCGCC
 CCTCGGGCGGCTCGGGGGCCGCATGGCGCGGGCCGCCGGCGCGCGCTGCCGCCGCCAGGCCGCCGTAGCGCCGCC
 CGCGCTAGGGCGGGCTGGCCTCCGTGGCGGGGGCAGCGGGCTGAGGGCGCGCGAGCCCTGCCGCCGCC
 GGCGCGGCC
 ATGGCGCGCGCGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC
 TGCTCGGGCTCGTCTGGCTCTGTGCTGCCCTCGCGCTCGTCTGCCGCCGCCGTAGCGTGAAGCGAGCG
 GCCCACGGCGCCGCCAGCCCCGAGGGCTGCCGGTCCGGGAGGCCGCCGCCGTAGCGCCGCCGCCGCC
 GCGATGCCGCCGGGGCAGCTCTGGCCGCCGCCGTGGACCCAGATGGCGGCCGCCGACAGGAACCTTCCT
 TCGTGGAGTCATGACGCCAGAAATACCTGCAGACTCGGGCGTGGCCCTACAGAACATGGCCAAGACAA
 TTCTGGAAAGTTAGTCTCAAGTGAGGGTCTGACACATCTGTACCAATTCCAGTAGTGCACACTACCGG
 GTGTGGACGACTCCTACCCGCCAGAAGAAGTCCTCATGATGCTCAAGTACATGCACGACCAACTTGGACA
 AGTATGAATGGTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAAACTCCTGAGGAGTT
 TGAACAGCAGCGAGCCCCCTTTCTGGCAGACAGGCCCTGGCACCGAAGAAATGGAAAATGGCCCTGG
 AGCGCTGGTGAGAACATCTGCTGAGGGGGGCCCTGGCGATCATGAGCCGGAGGTGCTCGGAGAATGGTGC
 ACATGGCAAGTGTCTCGGGAGATGTACACCACCATGAGGACGTGGAGGGTGGAGGTGTGCTCGGAGGTTG
 CAGGGGTGAGTGTCTGGTCTTATGAGATGCGGAGCTTTTATGAGAATTACGAGCAGAACAAAAAGGGT
 ACATTAGAGATCTCCATAACAGTAAACAGTACATCACATTACACCCAAACAAAAACCCACCCCTACCAAGT
 ACAGGCTCCACAGCTACATGCTGAGCGCAAGATATCGAGCTGCCCATCGCACAAACAGCTGCC
 TTGTCTGATGAGCAAATACAGCAACACAGAAATTCAAAAGAGGACCTCCAGCTGGAAATCCCTCCCTCCTCA
 TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGAATGGAGTTCTGACTGGAAAATACTTGTATTGGCAG
 TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAAGCCTGGACGACATTGT
 CATGAGGTCA
 TGGAGATGATCAATGCCAACGCAAGACAGAGGGCGCATCATGACTCAAAGAGATCCAGTAGGGCTACGCC
 GGGTGAACCCCCATGATGGGCTGAGTACATCTGGACCTGCTGCTCTGTACAAAAGCACAAAGGGAGAAA
 TGACGGTCCCTGTGAGGAGGCACCGTATTACAGCAGACTTCAGCAAAATCCAGTTGTGGAGCATGAGGAGC
 TGGATGCACAAGAGTTGCCAAGAGAAATCAATCAGGAATCTGGATCCTGTCTTCTCAAACCTCC
 TAAGA
 AGCTCGTCCCTTCAGCTCCCTGGTCAAGAGTGTGAGCACAAAGAACCCAAAGATAAAAGATAAACATACTGA
 TTCTTTGCTGGCGTTGACATGTTGTGAGATTATGGAAACTTGAGAAGACGTGCTTATCCCCAATC
 AGAACGCTCAAGCTCGTGGTCTGTTCAATTCTGACTCCAACCTGACAAGGCCAACAGTTGA
 ACTGATGA
 GAGATTACCGCATTAAAGTACCTAAAGCGACATGCAAGATTGCTGTGAGAGTTCAAGAGGCC
 CCCTGGAGTAGGATCCTCCCAGTTAACATGAATCTTGTCTCTCTCGCACGTCGACCTCGT
 GTTACTA
 CAGAATTCTTCAGCGATGCGAGCAAAATACAGTTCTGGGCAACAAATATTCTTCAATCATCTCAGGCCAGT
 ATGACCCAAAGATTGTTATAGTGGAAAGTTCCAGTGACAAACATTGCTTACTCAGAAAACATGGCTTCT
 GGAGAAAATATGGGTTGGCATCAGTGATTTATAAGGGAGATCTTGCCGAGTGGGCTTGATGTTCCA
 TCCAAGGCTGGGGCTGGAGGATGTGACCTTTCAACAAGGTTGTCCAGGGCAGGTTGAAGACGTTAGGAGCC
 AGGAAGTAGGAGTAGTCCACGTCACCATCTGTCTTGTGATCCAATCTGACCCAAACAGTACAAAATGT
 GCTTGGGGTCAAAGCATCGACCTATGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCAA
 GTTACAGAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCAGCTTGTGAGGAAAGACGTTT
 TAATTATCTAATTATTCTAACAAAATTGTTGATGATCAGTTTGAGTCCGTATAACAAGGATATATT
 AACAGGGTTTCTTACATAGGACTCCTTAAGATTGAGCTTCTGAACAAGAAGGTGATCAGTGTTGC
 CTTGAA
 CACATCTCTTGCTGAACATTATGAGCAGACCTGCTTAACCTGACTGAAATGTACCTGATGAACAAA
 ATT
 TTTAAAAAAATGTTCTTGTGAGACCTTGTCCAGTCCTATGGCAGAAAAGTGAACATTCTGCAAAGTAT
 TATTGTAACAAAACACTGTAACTCTGGTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTAC
 CTGTTGTT
 GTTTGTCTTCTTCTTACATTGTTAAAGCCATTCTGAGTCCAGGGCTGAGAAGGAGCTC
 CACTCTGTTACCCAGGCTGGAATG
 CAGTGGCGCAATTCTGGCTCATTAAACCTCCTGGTCAAGCAATTCCCTGCCCTGGCTCCCGAGT
 AGCTGGGATTACAGGCACACACCACGCCAGNTAGTTTTGTATTAGTAGAGAGACGGGTTTACCAT
 GCAAGCCAGCTGGCCACGTAGTTAAAGCAAGGGCGTGAAGAAGGCCAGTGAGGATGTGGCT
 GTCTCG
 TGGTAGTCATTGGCCTAAATAGACCTGGCATTAAATTCAAGAAGGATTGGCATTCTCTTGT
 GACCCCT
 CTCTTAAAGGGTAAATATTAGTTAGAATGACAAAGATGAATTATTACAATAAATCTGATG
 ACACAGACT
 GAAACATACACACATACACCCCTAACAAACGTTGGGAAAATGTATTGTTGTTCTT
 CATCCTGCTG
 TGTATGTTGAGATGGTTCTTACATTCTTCAATTACTGTTGTTTATCCTTGTATCTGAA
 ATACCTTAA
 TTTATTAAATCTGTTGTCAGAGCTGCTGCCATTCTGAGTACCTGTTAGTTAGTATT
 ATTATGTTGATCG
 GAGTGTGTTAGTCTGTTTATTGAGTAAACGATCTCCAAAGATTCC
 TTTGGAAACGCTTTCCCCTCC

FIGURE 143B

TTAATTTTATATCCTTACTGTTACTAAATATTAAGTGTTCTTGACAATTGGTGCATGTGTTGG
GACAAAAGTGAATGAATCTGTCATTATACCAGAAAGTAAATTCTCAGATCAAATGTGCCTTAATAAATTGTT
TTCATTTAGATTCAAACAGTGATAGACTGCCATTAAATACACGTCAATTGGAGGGCTGCGTATTGTAAATAG
CCTGATGCTCATTGGAAAAATAAACCGAGTGAACAATATTTCTATTGACTTTGAACCATTGTCTCATT
ATTCCCTGTTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTTAAACACGAAAAAA

FIGURE 144

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVILGFVLASRLVLPRASELKAGP RRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGRDRNLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPPIPVPVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRAADDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPKNPP
YQYRLHSYMLSRKISELRHRTIQHLREIVLMSKYSNTEIHKEDEQLGIIPPSFMRFQPRQREE
ILEWEFLTGTGKYLysAVDGQP PRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQQ
GYRRVNPMYGAEYILDLLLKYKKHGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVP SDNHF AFT
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACC GTT GCTGGGTGTC CAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTT CGGC TTGAGGTCCCAGCCTGGTGGCCCCAGGACGTTCCGGT CGCATGGCAGAGTGCT
 ACGGACGACGCCTATGAAGCCTTAGTCCTCTAGTTGCGCTTGCTATGGCCTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTGAATCATTATATA
 CAAGTTTAGAGAACCTAGTACGAAGTGTCCCTCTGGGGAGCCAGGT CGTGAGAAAAAATC
 TAACTCTCCAAAACATGTTATTCTATAGCATCAAAGGGATCAAATTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTAACCAATCCTATCAGTGAAGAAACTACA
 ACTTCCCTACAGGAGGCTTCACACCGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAAACATGTTCCATTGTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAACAAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAAACCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTGAAAAAAATTTAGATATTAATTACAAGTGCAACAGGCAC TTCTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAAGCAAGCC
 TTGCTCTAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTACATGCTGTGAATTC
 TAGATCTAAACTCTATGAATATTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTATTAAACAATAATATAAAATTAAACCTACTTGATATTCCATAACAAAGCTGA
 TTTAAGCAAAC TGCA TTTT CACAGGAGAAATAATCATATTGTAATTCAAAGTTGTAT
 AAAAATATTTCTATTGTAGTTCAAATGTGCCAACATCTTATGTGTATGTGTTATGAACA
 ATTTCATATGCACTAAAAACCTAATTAAAATTTGGTTCAAGGAAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKNSPK
HVYSIASKGSKFKELVTHGDASTENDVLNPISEETTFPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEPYIENEEPEPEPAAKQTEAPRMLPVVTESSTS PYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYKSQLLPGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCTGCCTGAGACAGCTGGCCTG
 ACCTCAAATCATCCATCCACCCCTGCTGTCATCTGTTTCAAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GCTTTGTGCTCATTTGGTCTCAGTTCTACGAGCTGGTGTCAAGGACA
 GTGGCAAGTCACTGGACGGGCAAGTTGTCAGGCCCTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCCTGTTCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAACTGAGTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGC
 TAAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGTGCTGGTCAAGTCCCAGATTAC
 GATGAGGAGGCCACCTGGGAGCTGGGGTGGCAGCACTGGGCTCACTCCCTCATTTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTCCCCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGCACAGGATTGTCTTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTCCAGCCCTCACCTGGCGCTGGCTCTATTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTCATGGGATGATAATTGTTCTCAAATCCAAGGGAAAATCCA
 GGCAGAACCTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCGAAGCTCTGCCTTGATCTGAAA
 ACTGTAACCCATAGAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGAGTGTGCGGATGACGTAGACAGGGGAAAGAACATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTCAC
 ATTCAATCCCCATTTATCAGCCTCCCCCCCAGCACCCCTCTACACGAGTAGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTCAATACAAATGACCAGTCCCTATTTTAC
 CTGCTGACATGTCAGTTGAAGGCTTGTGAGACCCCTATATCCAGCATGCGATGTGACGA
 GGAAAAGGGACTCCATATTCAATGTCCAGTGTCTGGGAT**TGAG**ACAGAGAACCCCTG
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCCTCCGACAGGTGGC
 CCCAGCTCCTCTCGGAGCCTGCGCACAGAGTCACGCCCTACTCTCCTTAGGGAGC
 TGAGGTTCTCTGCCCTGAGCCCTGCGCAGCAGGGCAGTCACAGCTCCAGATGAGGGGGAT
 TGGCCTGACCTGTGGGAGTCAGAACGCATGGCTGCCCTGAAGTGGGACGGAATAGACTCA
 CATTAGGTTAGTTGTGAAAACCTCCATCCAGCTAACGATCTGAACAAGTCACAACCTCC
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTGCCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTTGAGGTTGAGGGCACAGTGTTGCTAATGATGTGTTTTA
 TATTATACATTTCCCACCAAACTCTGTTGCTTATTCCACATTAATTACTTTCTCTA
 TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTGTGAGGCTCAAAGAATAAGAG
 GAGGTAGGATTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG
 AAAACAGAAGAGAGAAGGAAACTACAGGTCCATATCCCTCATTAAACACAGACACAAAAAA
 TTCTAAATAAAATTAAACAAATTAAACTAAACAAATATATTAAAGATGATATATAACTACT
 CAGTGTGGTTGTCCCACAAATGCAGAGTGGTTAATATTAAATATCAACCAGTGTAAATT
 CAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFKVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAAL GSLPLISIVGYVDGGIQLLCLSSGWFQOPTAKWKGPQGQDLSSDRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLI GETFFQPSPWRLASILLGLLCALC
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAE LR DARK HAVE VTLD PETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKS VVASQGFQAGRHYWEVDVGQNVG WYVGVCRDDVDRGKNNV TLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTCATTGCTGGTGGCA**ATG**ATGTATCGGCCAGATGTGGTGGGGCTA
 GGAAAAGAGTTGTTGGGAACCTGGGTTATCGGCCCTCGTCATCTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTATTATGTGAGATATAATCAAAGAACGACTACAA
 TTACTATAGCACATTGTCAATTACAACGTACAAACTATATGCTGAGTTGGCAGAGAGGGCTT
 CTAACAATTTACAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTATAAA
 TCTCCATTAAGGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTCAAGTCAACAGAACGATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAAATTGTTCAACTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCTAAAGTA
 GATCCTCACTCAGTAAAATTAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAAACCTAGGTCAAGACTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGCCCTGGCAGGCTAGCCTGCAGTGGGATGGAGTCATCGCTGT
 GGAGCAACCTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTACAACATATAA
 GAACCCTGCCAGATGGACTGCTCCTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCATGAAAATACAAACACCCATCACATGACTATGATATTCT
 CTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGA
 TGCAATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAA
 ATGATGGTTACAGTCAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACACTGGTTAGTTCAAGATGCTA
 GAGATATCTGGTACCTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG
 CCTGGTGTAACTAGAGTTACGGCCTTGCAGGACTGGATTACTTCAAAAACTGGTATCT**TA**
AAGAGACAAAGCCTCATGGAACAGATAACATTGTTTGTGTTTGGGTGTGGAGGCCATT
 TTTAGAGATAAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTTGCTGATGCATGTATTTCTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGCATCTGTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTGATTCATTGTTCTCTAGAAGTTGTGAGAATTGAC
 TTGTTGACATAAATTGTAATGCATATACAATTGAAAGCAGCTCCTTCTTCAGTTCCCT
 AGCTCCTCTCATTCAGCAAATATCCATTGCAAGGTGAGAACACAAGGAGTGAAGAAAATA
 TAAGAAGAAAAAAATCCCTACATTGAGGACAGAAAAGTATTAGGTGTTTCTTAGT
 GGAATTAGAAATGATCATATTGATTGAAAGGTCAAGCAAAGACAGCAGAACATACCAAC
 ACTTCATCATTAGGAAGTATGGAACTAAGTTAAGGAAGTCCAGAAAGAACGCAAGATATA
 TCCTTATTTCTTCAACAACTACTATGATAAATGTGAAGAACAGATTCTGTTTGTG
 ACCTATAATAATTACAAACTTCATGCAATGTTACTGTTCTAAGCAAATTAAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAACCCCA

FIGURE 150

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTCCAGCAAACGGCATTGAAGTTGAAGATAACAACCTGACAGCA
 CAGCCTGAGATCTGGGGATCCCTCAGCCTAACACCCCACAGACGTCACTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGCTCTCCCTGCCTCTGTGGCTCTGGC
 CGTGACCTTCTGGTCCCAGAGCTCAGCCCTTGGCCCTCAAGACTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCCTTGCCGGCTGTCCCCTGCAGACTACGACCAC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGCCGGCCTGCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCATGGGAGAAGTGCGCATTGCC
 CCGAAGAGGGCCCGCAGTGGTCACTGGTGTGCCCTCTCCCCGGTCCACTACTGG
 CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCGCTGAACGCTACGGTCC
 CAGAGCCGAACGTAGAGGGCTGAAGCCAGGGGCATTATGTCGTTGCGTAGTGGCCGCTA
 ACGAGGCCGGGCAAGCCCGTGCCTGCCAGGCTGGAGGAGAGGGCCTCGAGGGGCCGACATC
 CCTGCCTCGGGCCTTGCAGCCGCCCTGCCGTGCCCTGCTAACGCTGTGCCGCCCTGGTGTGGCA
 GGCGTCGGGGTGGGCACGGCCCTGCCCTGCTAACGCTGTGCCGCCCTGGTGTGGCA
 GCCTGCGCGATCGCTGGGCTGCCGCCGAGCCGCCGCCAGCCGCAGGGCGCTC**TGA**
 AAGGGGCCTGGGGCATCTCGGGCACAGACAGCCCCACCTGGGCGCTCAGCCTGGCCCC
 GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGAGGCCAG
 GCTCCAGGGCCACGGCGGAGTCATGGTCTCAGGACTGAGCGCTTGTAGGTCCGGTACTT
 GGCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTA
 AGCGGCCAGATAATAATAATGTAACCTTGCGGTTAAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADI PAFGPCSR
AVPPNPRTLVHAAVGVGTALALLSCAALVWHFCLRDRWGCPRAAARAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCGCGAAGAAGTTCC
 CTGCCCGATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGCACCGGG
 CCCAGCGCCGACGATCGCTGCCGTTTGCCCTGGGAGTAGGATGTGGTGAAGGATGGGGC
 TTCTCCCTTACGGGGCTACA**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCCTGCCTGCT
 CTACGCCCTCAATCTGCTTTGGTAATGTCCATCAGTGTGGCAGTTCTGCTTGG
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACAGGAGGTAGAGGAAGCAGTC
 ATTTGACTTACTTCCTGTGGTCATCCGGTCATGATTGCTGTTGCTGTTCTTATCAT
 TGTGGGGATGTTAGGATATTGTGAAACGGTAAAAGAAATCTGTTGCTTGCATGGTACT
 TTGGAAGTTGCTTGTCACTTCTGTGAGAACTGGCTTGTGGCGTTGGACATATGAACAG
 GAACTATGGTCCAGTACAATGGTCAGATATGGTCACTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGAATTTCAGAGAGAGTTAAGT
 GCTGTGGAGTAGTATATTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCAAACAGGCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGGGAAGAAAATGTATTCTTTGAGAGGAACCAAACAATGC
 AGGTGCTGAGGTTCTGGGAATCTCATTGGGTGACACAAATCTGGCCATGATTCTCAC
 ATTACTCTGCTCTGGCTCTGTATTATGATAGAAGGGAGCCTGGACAGACCAATGATGTC
 CTTGAAGAATGACAACACTCAGCACCTGTCACTGCTTCACTGAGATGGAG
 TGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAATACACACTTGAGATGGAG
 GAGTT**TAA**AAAGAAATGTCACAGAAGAAAACCACAAACTGTTTATTGGACTGTGAATT
 TTTGAGTACATACTATGTGTTTCAAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTAAATGAGGATGGAAAAGTTCTGATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTC
 CTGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATTTC
 CGCATCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTTGATTACTT
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATAACTAATA
 ACTTTATTACTCAGCGATCTATTCTCTGATGCTAAATAAAATTATATATCAGAAAATTT
 AATATTGGTGAACACATTGTCTAACAGCTGATCAGGGATTGGTACTAAATATTCTACCACTAAAA
 GAGCAAGCTAACACATTGTCTAACAGCTGATCAGGGATTGGTACTAAATATTCTACCACTAAAA
 TCTGTATAATTCACTGATTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
 ATTTGCTCTGTATAGCATCATTATTTAGCCTTCTGTTAATAAAGCTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTAAATCTAACACTAATTGAAAATTAA
 CCAGTGTGATACATAGGAATCATTTCAGAATGTTAGTCTGGCTTTAGGAAGTATTAAATA
 GAAAATTGACACATAACTTAGTTGATTCAAGAAGGACTTGTATGCTGTTCTCCCAAATG
 AAGACTCTTTGACACTAAACACTTTAAAAAGCTTATCTTGCCTCTCCAAACAAGAA
 GCAATAGTCTCCAAAGTCAATATAAATTCTACAGAAAATAGTGTCTTTCTCCAGAAAAAT
 GCTTGTGAGAATCATTAAACATGTGACAATTAGAGATTCTGTTTATTCACTGATTA
 ATATACTGTTGGCAAATTACACAGATTATAAATTGTTACAAGAGTATAGTATATTATTT
 GAAATGGGAAAAGTGCATTTACTGTATTTGTGTTATTCTCAGAATATGGAA
 AGAAAATTAAATGTGTCAATAATATTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVYYFTDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFGLGISIGVTQILAMILTITLLWAL
YYDRREPDTDQMMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTGCTCAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCC
 TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCAGCCAGGA
 CCTGTGTGGGAGGCCCTCCTGCTGCCTGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATG**TACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCATCAAGG
 TGATTCTGGATAAATACTACTTCCCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCTGGGGAGGACGAGGAGCAGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGAACTGGTCTCTGCCTGTTGACAACACTCACAGAACGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTCGCATGCGGAACACTCAAGTGGCCCTGTC
 TCTCAGGCTCCCTGGCTCCCTGCACTGTCTGCCTGTTGGAAAGAGCCTGAAGACCCCCCGT
 GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATTCTGGACCCCCACTGGTCCTCACGGCAGCCCAC
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGC
 AGCTTCCCATCCCTGGCTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACCCAA
 AGACAATGACATGCCCTCATGAAGCTGCAGTCCCACTCACCTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGA
 TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTATTGACAGCACACGGTCAATGCAGACGATGGTACCGAGGGAAAGTCACCGAGAAAGA
 TGATGTGTGCAAGGCATCCGGAAAGGGGTGTGGACACCTGCCAGGGTACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAAGTGGCATGTGGTGGCATCGTAGCTGGGCTATGGCTGCC
 GGGCCGAGCACCCAGGAGTATAACCAAGGTCTAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAAT**GCTGCTGCCCTTGCACTGCTGGAGGCCCTGGTACACCC
 CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTGGTACACCC
 CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGCCCTCAATTCTGTAAGAGACCC
 TCGCAGCCCAGAGGCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTGGTGTCCCC
 AGCATCCCAGGGAGAGACACAGCCCACAGAACAGGTCTCAGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGAAAAGCCCAGATCACTGTGG
 CTGGAGAGGAGAAGGAAAGGTCTGCCAGCCCTGTCCGTCTCACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACC
 ACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIKVILDKYVF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELRMNRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC CGGSILDPHWVL TAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDGGPLMYQSDQWHVVGIVSWG YGC GGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCAGTGGAGAGACCGGAAAGCCTGGCATTCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCAG
 AGCTCCCTGGTACAGTCTGGCTGAGC**ATGGCC**CTCCCAGCCCTGGACCCCTGGAGCCTCCTGGCC
 TTTCCCTTCAACTGCTCAGCTGCTGCCGACGACGCCGGGGAGGCAGGGCCATGCCA
 GGGTCAGATACTATGCAGGGATGAACGTAGGGACTTAGCTTCTTCCACAGAAGGGCCTCCAGGATTTGACA
 CTCTGCTCCTGAGTGGTATGAAATACTCTCACGTGGGGCTCGAGAACGCATTCTGGCCTGGATATCCAGG
 ATCCAGGGTCCCCAGGCTAAAGAACATGATACCCTGGCCAGCCAGTGACAGAAAAAGACTGAATGTGCCTTA
 AGAAGAAGAGCAATGAGACACAGTGTTCAACTTACATCCGTGCTGGTTCTTACAATGTCACCCATCTCTACA
 CCTGCACCTCGCCTTCAGCCCTGCTTACCTTATTGAACTTCAAGATTCTACCTGTTGCCCATCTCGG
 AGGACAAGGTATGGAGGGAAAGGCCAAAGCCCCTTGACCCGCTCACAAAGCATAACGGCTGCTTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTCCTGGCAGTGAGCCATCCTGATGCGCACACTGGATCCCAGC
 CTGTCCTCAAGACCGACAACCTCCTCCGCTGGCATCATGACGCCCTTGTGGCAGCCATCCCTCGACCC
 AGGTCGCTACTTCTTCGAGGAGACAGCCAGCGAGTTGACTCTTGAGAGGCTCCACACATCGGGTGG
 CTAGAGCTGCAAGAATGACGTGGCGGGAAAAGCTGCTGCAGAAGAAGTGGACCACCTCCTGAAGGCCAGC
 TGCTCTGCACCCAGCGGGGAGCTGCCCTCACGTCATCCGCCACGCGCCTGCTCCCCGCCATTCTCCA
 CAGCTCCCCACATCTACGCAGTCTTCACCTCCAGTGGCAGGTTGGCAGGACAGGAGCTTGCGGTTGTGCCT
 TCTCTCTTGGACATTGAACGTGTCTTAAGGGAAATAACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA
 CTTATAGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCTCCTGTATAAGGCCCTGACCT
 TCATGAAGGACCATTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAATCTGGCGTGGAGTATA
 CACGGCTTGCAGTGGAGACAGCCAGGGCCTTGATGGCACAGCCATTTGTCATGTACCTGGGAACCACACAG
 GGTCGCTCCACAAGGCTGTGGTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTAGCTGTTCCCTGACC
 CTGAACCTGTCGAAACCTGCACTGGCCCCACCCAGGGTGCAGTGTTGAGGCTCTCAGGAGGTGTGG
 GGGTGGCCCGAGCCAAGTGTAGTGTCTATGAGAGCTGTGGACTGTGTCCTGCCGGGACCCCCACTGTGCCT
 GGGACCCCTGAGTCCGAACCTGTCCTGTCTGCCCTGGACCTGAACCTGGAAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGCATGTGCCAGTGGCCAGTGGCCCTCAGAGCCGCCGAAATCATTA
 AAGAAGTCTGGCTGCCCCAACTCCATCCTGGAGCTCCCTGCCCTACCTGTCAACCTGGCTCTTATTATT
 GGAGTCATGGCCAGCAGCAGTCCCAGAACCTCTTCACTGTCTACAATGGCTCCCTTGCTGATAGTCAGG
 ATGGAGTTGGGGTCTTACCAAGTGTGGCAACTGAGAACATGGCTTTCATACCTGTGATCTCTACTGGGTGG
 ACAGCCAGGACCAGACCTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTGA
 CCAGGGTCAGTGGTGGGCCCTGGCTGCCAGCAGTCCTACTGGCCCTACTTGTCACTGTCACTGTCT
 TTGCTTACTGCTTCAAGGACCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGCTGGGCAAGG
 TTCAGGGCTGTGAGACCTGCCCTGGGAGAAGGGCCGTTAACGAGAGCAACACCTCCAGTCTCCCAAGG
 AATGCAGGACCTCTGCCAGTGTGGACGCTGACAACAACTGCCCTAGGCAGTGAGGTAGCT**TAA**ACTCTAGGCA
 CAGGCCGGGCTGCCGTGAGGCCAGTGGCATGCTGGCTGGGCCCAAGCACAGCCCTGACTAGGATGACAG
 CAGCACAAAAGACCACCTTCTCCCTGAGAGGAGCTCTGCTACTCTGCACTGATGACACTCAGCAGGGTG
 ATGCACAGCAGTGTGCTCCCTCATGGACTCCCTACCAAGCAGCATGAGCTCTAACAGGGGGCTAC
 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTCAGTCTGGCATTCCAGGGACCC
 CAGAAACACAGTGTCAAGAGACCTAAAAACCTGCCCTGTCCCAGGACCCATGGTAATGAACACCAAACATC
 TAAACAACTCATATGCTAACATGCCACTCTGGAAACTCCACTCTGAAAGCTGCCCTGGACACCAACACTCC
 TCTCCCAAGGGTATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAAGTGTGCAACCGCTGACTCC
 TTTGCTGAAGTGTGACCCACCTTCTTCTGCTTCAGTTGGGAGACTCTGATCCCTCTGCCCTGGCAGAATGG
 CAGGGGTAATCTGAGCCTCTTCACTCCTTACCTAGCTGACCCCTCACCTCTCCCCCTCCCTTTCTTGT
 TTTGGGATTGAGAAAATGCTTGTGAGAGACTGTTATTTTATTAAAAATATAAGGCTTAAAAAA

FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQQLQLLLPTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFF
ETASEFDFFERLHTSRVARVCKNDVGGEEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFIMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPEPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSILRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTAGCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGGCTTCCGTAGAAG
 TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTAGTGGCTTCCTCCCTGGGTCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGGCCATTATCTACTGATGGA
 CCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTAACCAAAAGAG
 GTCCTTTATGCCAGATTTAAAAGGAAGAAAAATCATATCAAGTTACAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTCTTCTGGAAGAAACTTTAGG
 TGGCAGAGGAAAATTGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTAAATAGAAAGGATATCATGGATTCCCTAAAGAATGAGAACTTCGACATGGTGATA
 GTTGAAACTTTGACTACTGTCCTTCTGATTGCTGAGAAGCTGGGAAGCCATTGTGGC
 CATTCTTCACTTCATTGGCTTTGGAATTGGCTACCAATCCCCCTGTCTTATGTC
 CAGTATTCCGTTCTGCTGACTGATCACATGGACTCTGGGCGAGTGAAGAATTCTG
 ATGTTCTTAGTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTGACAACACCATCAA
 GGAACATTCACAGAAGGCTTAGGCCAGTTGTCATCTACTGAAAGCAGAGTTGT
 GGTCATTAACACTGACTTGCCTTGATTGTCGACCTGCTTCCAAACACTGTTAT
 GTTGGAGGCTTGATGAAAACCTATTAAACCAGTACCAAGACTGGAGAACATTGATTG
 CAAGTTGGGACTCTGGTTTGTCCTGTGACCTGGCTCCATGGTAACACCTGTCAGA
 ATCCGAAATCTCAAGGAGATGAAACATGCCTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCACTGTTCTCATTGGCCAAAGATGTCACCTGGCTGCAAATGTGAAAATTG
 CTGGCTCCTCAGAGTGCACCTGGCTCACCAAGCATCCGTCTGTTGTCACCCACGGCG
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCTCTTT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAACGCCAAAAGTTGGTGTCTATTGAGTT
 AAAGAAGCTCAAGGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGGCAGTGGCTGCCAGTGTCTGCACCTGGCTCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGCTGGATTGACCACGTCCCTCAGACAGGGGCGGACGCACCTCAAGCCCTA
 TGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTCGACGTTTGTTGTCGCTGGC
 TCACTCTGGGACTCTATGGCTTGGAAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACAT**AA**GGCCAGGTGCAGCCTGGCGGGGCTGTTGG
 GCGATGTCACCATTCTAGGGAGCTCCCACAGTTCTGGCAGCCCCATTCTCTAGTCCTC
 TAGTTATCTCCTGTTCTGAAGAACAGGAAAATGCCAAAATCATCCTTCCACTG
 TAATTTGCTACAAATTCTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT
 CTTGTCCTCCTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGCTCTGAGTGACTTG
 GACCACTGACCCCTCAGATTCCAGCCTAAACATCCACCTCCTCTCATGCGCCTCTCCGAA
 TCACACCCCTGACTCTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCACTCCTGCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTCTTCAGTTCTGTT
 TGTCTCCCACATATTCTCTTAATGCTCAGGAAGCCTGCCCTGTGCTGAGAGTTCA
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCTGTCTGGTGCCCACAGTGAGCTC
 TCTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTCTGAAAGAAAATAAAGTTACA
 GCGTTATCTCTCCCCAACCTCACTAA

FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLGVFLLPGVILLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIDMSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFARPLLPTVYVGGLMEKPIKPVQPQDLENFIAKFGDSGFVLVTLSMVNTCQNP
EIFKEMNNAFAHLPQGVIWKCQCSHWPKDVLAAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPLFGDQOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLGLT
LGTLWLCGKLLGMAVWWLRGARKVKET
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGGATTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTACACACACATACCATGTT
CTCCATCCCCCAGGTCCAGGCCCTCAGTGTCCCCTACAGCAGGGCTACCTGAAGCTCT
GGCTCAGGCCCTCCCGTCCAGTGGCAGGGGGCTCATCCCTCTTCTCTCCAAAGCCCA
ACTGCTGTCAGTGCATGCTCTGCCAAGGAGGAGGAAC TG CAGTGACAGCAGGAGTAAGAGT
GGGAGGCAGGACAGAGCTGGACACAGGTATGGAGAGGGGTTCAGCAGCCTAGAGAGGGC
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA
AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTGGGAGCCAAGCCACACTGGC
TACCAGGTCCCCACACAGTCCCAGGCTGCCCTGGTTCTGGTGTCTGGCCCTGGGGGCC
GGGTGGGCCAGGAGGGTCAAGAGCCCTGTCTGGAGGGGAGTGCTGGTGTCTGTGA
GCCTGGCCGAGCTGCTGCAGGGGGCCGGGGAGCAGCCCTGGAGAGGCACCCCTGGGC
GAGTGGCATTGCTGCCTCCGAAGCCACCATGAGCCAGCAGGGAAACCGGCAATGGC
ACCAGTGGGCCATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTGACCGGGC
CTCTGGCTCCTCGTAGCCCCGTCCGGGTGTCTACAGCTCCGGTCCATGTGGTGAAGG
TGTACAACCAGCAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCATCTCAGCC
TTTGCCAATGATCCTGACGTGACCCGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTGGA
CCCTGGGGACCGAGTGTCTGCGCCTGCGTCGGGAACTACTGGGTGGTTGAAATACT
CAAGTTCTCTGGCTCCATCTTCCCTCTTGAGGACCCAAGTCTTCAAGCACAAGAAT
CCAGCCCTGACAACTTTCTGCCCCCTCTGGCCCCAGAAACAGCAGAGGCAGGAGAGAG
ACTCCCTCTGGCTCTATCCCACCTCTTGCATGGGACCCCTGTCAAACACCCAAGTTAA
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTCCACCCACCCACCCCCAGTTAC
CTCCCAGCCACCTGCTGCATCTGTTCTGCCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA
AGAAGGAAGATCTGCACTACTTGCGGCCTGTCCGGTTCCCCACCCAGCTTCC
GCTCAATGCTGATCAGGGACAGGTGGCGAGGTGAGCCTGACAGGCCCCACAGGAGCCCAG
ATGGACAAGCCTCAGCGTACCCGTCAGGCTCTTCTGTGAGGAAAGCCAGCATCACGGATC
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGAGGCTCAGCCAC
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
GGCTGTCCTCTATGCTGGATCCCAGATGGACTCTGCCCTACCTCCCCACCTGAGATTAG
GGTGAGTGTTTGCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
ACCATGGAAAACATCGATAACCGATGCATCCTCTGCTGGCCACCTCCTGAAACTGCTCCAC
CTTGAAGTTGAACTTAGTCCCTCCACACTCTGACTGCTGCCTCCTCCCCAGCTCTC
TCACTGAGTTATCTCATGTTACCTGTCCCAGCATATCCCCACTATCTCTCTCCGTAT
CTGTGCTGCTTATCTCCCTCCTTAGGCTCTCCTTATTACCTGGGATCCATGATTCTATTCCTT
CAGACCCCTCTCCGTCCAGATGCTAAACCCCCCTCTCTTTCTTATCCCGCTGTCCCCAT
GGCCAGCCCTGGATGTAATCTAAAAACAACTAGAGAATGGTGGTCAGTGAGACACT
AGAATTACTTAAGGGAGGAAGATGCCTCTGGAGTTGGATCGGGGTTTACAGGTTACAAGTAGGT
TGTTGCAGAGGGAAAAAAAAATCAAAACCTGTTAACTAAAAAATTAAAAA

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32

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FIGURE 163

GCTGTTCTCGGCCACCACTGGCCGCCGGCGCAGCTCCAGGTGTCTAGCCGCCAGC
 CTCGACGCCGTCCGGGACCCCTGTGCTCTGCAGAAGCCCTGGCCCCGGGGCCGGGCAT
 GGGCCAGGGCGCGGGTGAAGCGGCTTCCCAGGGCGTGACTGGCGGGCTTCAGCC**CAT**
GAAGACCCTCATAGCCGCCTACTCCGGGTCTGCAGCGAGCGTCAGGCCAGGCTGACC
 GGAGCCAGCGCTCTCACGGAGGACCTGCAGCTGCGCAGGGGTCTGGAGATGGGGCACT
 GGATCCAGCATCCTCTCCGCCCTCAGGACCTCTCTGTACCTGGCTCAATAGGTCCAA
 GGTGGAAAAGCAGCTACAGGTATCTCAGTGCTCCAGTGGTCTGTCTTGTACTGG
 GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTATCGCTGTG
 CTCTACTTCACTGGCTGGTGTGACTGAAACACACCCAAGAAAGGTGGCAGGAGGTACA
 GTGGGTCCGAAACTGGGCTGTGGCGCTACTTCGAGACTACTTCCCATCCAGCTGGTGA
 AGACACACAACCTGCTGACCACCAGGAACATATATCTTGGATACCACCCCCATGGTATCATG
 GGCCTGGGTGCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTCCCAGG
 CATA CGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCTGTGTTGAGGGAGTACC
 TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGACACCATAGACTATTGCTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCATCGTGGTGGGGTGCAGCTGAGTCTTGAGCTCCATGCC
 TGGCAAGAATGCAGTCACCCCTGCGGAACCGCAAGGGCTTGTGAAACTGGCCCTGCGTCATG
 GAGCTGACCTGGTCCCCTACTCCTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTC
 GAGGAGGGCTCTGGGCCGATGGTCCAGAAGAAGTCCAGAAATACATTGGTTGCC
 ATGCATCTTCCATGGTCAGGCCTCTCTCCGACACCTGGGGCTGGTGCCTACTCCA
 AGCCCCATCACCACGTGTTGGAGAGGCCATCACCATCCCCAAGCTGGAGCACCCACCCAG
 CAAGACATCGACCTGTACCAACACCATGTACATGGAGGCCCTGGTAAGCTCTCGACAAGCA
 CAAGACCAAGTCGGCCTCCGGAGACTGAGGTCTGGAGGTGAAC**TGA**GCCAGCCTCGGG
 GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTGCTCTGTAATTGGAAAGTGTCA
 TGGGTGTCTGTGGTTATTAAAAGAAATTATAACAATTGCTAAACCAAAAAAAA
 AAAAAAAA
 AAAAAAAA

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNR
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVFDWNTPKKGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVIREYLMGGICPVSRTIDYLLSKNGSGNAIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVI FEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTGVGEPIТИPKLEHPTQQDIDLHYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGCCGGGATGGGGGCCGGGGCGCCGGCGCCACTCGCTGAGGCCCGACGCAGGCCGGCCGGGCC
GGCCGAGGAGCGCGCGGCCAGAGCAGGCCAGGGCAGCTGTCCCCTGGCTCTGCTGACCTGTGCCTTGA
CGCGCTGCAGGCTTGTCCAGCCGAAGCCCTGAGGCAGCTGTCCCCTGGCTCTGCTGACCTGTGCCTTGA
CGGCTGCCTCAGCGAGGGCGTGACCCGCTCCTGAGCAGCGCCATGGCCTGCTGGCTTCCGAAGACCCA
GTTCGTGCACCTGCTGGCTTGTCTCGTGGTAGTGGCTGGCATCAACTCGTCCAGCTGTGCAC
GCTGGCCCTCTGGCCGGTCAGCAAGCAGCTTACCGCCGCTCACTGCCGCTCGCTACTCACTCTGGAGCCA
ACTGGTCATGCTGCTGGAGTGGTAGTGGCTTGACACTGTTCACGGACCAGGCCACGGTAGAGCGCTT
TGGGAAGGAGCACCGCAGTCATCATCCTCAACCACAACCTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
GCGCTTGGAGTGTGGAGCTCAAGGTCTCGTAAGAAGGAGCTGCTTACGTGCCCTCATCGCTGGAC
GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGCCGGACACCGTGGTGAAGGGCTGAG
GCGCCTGTCGGACTACCCCGAGTACATGTGTTCTCCTGTACTGCGAGGGACCGCCTCACGGAGACCAAGCA
CCGCGTTAGCATGGAGGTGGCGCTGCTAAGGGCTCCTGTCAAGTACCGACCTGCTGCCGGACCAAGGG
CTTCACCAACCGCAGTCAGTCAGTCAGTGCTCCGGGACAGTCAGCTGTCTATGATGTAACCCCTGAACCTCAGAGGAAA
CAAGAACCGTCCCTGCTGGGATCCTCTACGGAAGAAGTACGAGGCGACATGTGCGTGAGGAGATTCCCT
GGAAGACATCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCGAGGAGAAGGACCGCCTCA
GGAGATATATAATCAGAAGGCATGTTCCAGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA
CTTCCTGTCCTGGGCCACCATTCTCCTGCTCCCTCTTCAGTTGTCTGGCGTCTTGCCAGCGGATCACC
TCTCCTGATCCTGACTTCTGGGTTGTGGAGCAGCTCCTTGGAGTTCGCAACTGATAGGAGAATCGCT
TGAACCTGGAGGTGGAGATTGCAGTGAGCTGAGATGGCATCACTGTAUTCCAGCCTAGGAAACAGAGCAAGACT
CAGTCTAAAAAAAAACAAAAACCCCCAGAAATTCTGGAGTTAACGCTCAGAGACCCATGGTGCACCGTCACCAAATCAA
ATTCACTAGAGGCTAACAGCAGATTGAGCAGGGCAGAAAAAAATCAGCAAGCTGAAAGATGGTACCTGAGATT
TTTCAGGCTAATGAAAAAGAATGAAGGAAATTAAACAGCCTCAGAGACCCATGGTGCACCGTCACCAAATCAA
CATATGCATGATGAGAGTCCCAGAAGGGAGAGGAGAAAGGTCAGAAAGAATGCCACAAGCTGATGAAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTCAT
AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTGTTCAAAGGATCTTG
ATCAGATTAACAGCTCATTCTCCTCAGAAATCATGGGAGCCAGGAGATAGGGATGAAACACTGTTGAAGGCAA
AACCTCAACTGTAATTATTGACTTTGAGCTTAGATGGCCTGACCTCTTGTCTCAGGGACAGTTTCA
ATTTAATCCCTAATAACAATTAGTCAGCTCCTGACCTGTAGGAAGGCCGTCTTAGGCCGGCACAGTGGC
TTACACCTGTAATCCAGCATTGGAGGCCAGACGGGTGGATCATTGGGTCAAGCTGATCTCAAACCT
GAGTTCAAGGTGATCTGCCGCCTCAGCCTCCAAAGTGTGTGATTGCAAGCTGAGCCACTGCCCTGGCCGGA
ATTTCTTTAAGGCTGAATGATGGGGCCAGGCACGATGGCTACGCCGTGATCCCAAGTAGCTTGGATTGTA
AACATGCACCAACCATGCCCTGGCTAATTGGTATTAGTAGAGACGTGTTAGCCAGGCTGGCTCGATCTCCT
GACCTCAAGTGACCACCTGCCCTCAGCCTCCAAAGTACTGGGATTACAGGCGTAGGCCACTGTCCTGGCCTTGA
GCATCTTGTGATGTGCTTATTGCCATTGGTATATCTCTATCTTGTGAGGAAATGCTGTTCAAAGTCCTTGA
CCTTTAAATTGTTATTATTATTATTGAGACAGGGCTTGTGTTCTGGCCAGGCTGGAGTA
CAGTGGCACAGTCTGGCTACTGCAGCCTGACCTCTGGCTGCAAGTGTGATCCTCCACCTCAGCCTCCCTG
AGCTGTATTGGTATTGAGCTGTAGTTGTATTGGAGACAGCATTTCACCATGA
TGCCCAGGCTGGCTTGAACCTGAGCTCAAGTGTGCTCAGCCTCCAAAGTGTGAGGATTACAGA
CATGAGCCACTGCACCTGGCAAACCTCCAAACATCAACACACACACACACACACACACACACACACACACAC
GAGGGGCCGGGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATGCTGGCATGAGAAGTCGAGGCTG
CACTGAGTCGAGGTTGTGCGACTGCAATTCCAGCCTGGACAAACAGAGTGTGAGACCCCTGTC

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVSVGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGRVRLIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTATTTAAGAACCTGAAGTACTATGCATCACTCCCTCCAATGTCTGGGGCA
 GCCACCAGGCATATTCATCTTGTTGTGTGTTCTTGTCTTAGCACTGGGGCACTTCTT
 GCTTATTCTTGGTAGGAAAGGGGCTCAGTTGTCTGTGGGGTGGCAGGCAGGCCG
 GCTTACGCCTGATAACGCCCTGGGTTAGAAGGGAAAGGGAAAGATAAACTTTATACAAATGGG
 GATAGCTGGGTCTGAGACCTGCTCCTCAGTAAAATTCTGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATACCCTGCTAAAGCCTCTCAGGGCTTCTCTGTTCTTAGGATCAA
 AGTATTAGAGCTACAAGAGCCCTCATGGCTGGCCCTGCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTGTCGTTCTGTAATGTGGTATGCCATGGGTCTTGACAAAGCCT
 TTCCTCTTGGCTGGACACTGTTCCCTGCCCTGCCCTACTCTTCTACTTAATATGTAGTC
 ATCCTGCAGATTCAATTCTAACATCATTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTTGTTAATGCTCTCATAGACCACTTGTGTTCCCTTGCAGCACTGCCACTCAGTTGTA
 TCTTATGTGCGTTGTGGTTGTATGGTTGTCTGTTCCCAGAATGCCAGCTCTGAGC
 TGCAGGGTCAAGGGCATTGCTGTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
 CATGTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAGATTGAAATCTCAGTTCACCA
 GATGGTAGGGCCCAGCATTGAAATTACACAGTTGACTGTGCTGTGAATTATCTGGGA
 TGCAGGTCTGATTCACTAGGCCCAGGTTGGCATCTCTAACAAACTCCCACGTGATGCTGA
 TGCTGGCCTATGAACTATAACTAAATAGTAAGAACATCTATGGAGCCAGGCTGGCATGGTGGC
 TCACACCTATGATCCCAGCACTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAACATCGCTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHSLQCPGAATRHIHLCVCFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWRR
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPEWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTGGCCTCTGAACAACTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAAC TGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAAAATCTGTTTTGTTCTTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTACGTCTGGAGGCAGTGACTCGGGAGTGCAGGTAGCTGAGCCTTGGTA
 GCTGCGGCTTCAAGGTGGCCTGCCCTGGCGTAGAAGGGATTGACAAGCCGAAGATT
 CATAGGCGATGGCTCCACTGCCCAAGGCATCAGCCTTGCTGTAGTCATCACTGCCCTGGGG
 CCAGGACGGCGTGGACACCTGCTCAGAACAGTGGTGAGACATCACGCTGCCGCCCAT
 CTAACCTTTCATGTCCTGCACATCACCTGATCCATGGCTAATCTGAACCTGTCCCAAGG
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAAGGAACTTGTGCCAAATTATGGGTAGAAAAGATGGAGGTGTTGGGTATCACAAGGC
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGAAAGGGCTGCCGATGGCGATGACACACT
 CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGATCCACGTACCAAGCTGCTG
 AAGGGCAACTGCAGGCCATGCTCATCAGCCAGGCAGCAGCCAAATCTGCGATCACCAG
 CCAGGGCAGCCGTCTGGAAAGGAGCAAGCAAAGTGACCAATTCTCCTCCCTCCTCCCTC
 TGAGAGGCCCTCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGCTAATG
 GCTCAGTGTGGCCAGGAGGTCAAGCAAGGCCTGAGAGCTGATCAGAACGGCCTGCTGTGCG
 AACACGGAAATGCCCTCCAGTAAGCACAGGCTGAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTTATAACCCAGGAGACTTGATTGAATTGAAACCCCCAAA
 TCCAAACCTAAGAACCAAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
 CCAACATTTGGGAGGCCAGGCGGGTAGATCACCTGAGGTCAAGGAGCTTCAAGACCCAGCCTG
 GCCAACATGGTGAACCCCTGTCTACTAAAAAATACAAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTGAAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATTACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSILYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLAALTRAVQVAEPLGSCGFQGGPCPGRRD
```

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCGGCCATGACCCAGCCGGTCCCCGGCTCTCCGTGCCGCCGCCGCT
GGCCCTGGGCTCAGCCGACTGGCGCCGCCCTCGCCACTGGCCTCTTCCCTGGGGAGGCGGT
GCCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCAGGGAGCACCAGGCGCTGCGAAGCCTGAGGCTGCTGAC
CCTGGAGCAGCCGCAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTGGCCAACC
TGGCGCGGCTCATCCAGGCCAAGAACGGCGCTGGACCTGGCACCTCACGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCGCCGGACGGCGCGTGGTACCTGCGAGGTGGACGCCA
GCCCGGAGCTGGGACGGCCCTGTGGAGGCAGGCCGAGGCCGAGCACAGATGCCCTCC
GGCTGAAGCCGCCTGGAGACCCCTGGACGAGCTGCTGGCGGGCGAGGCCGGCACCTTC
GACGTGGCCGTGGATGCGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCCTCAGAGTCCTGTGGCGGGGAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCAAACCTAAACGAACGCATCCGGCG
GACGTCAGGGTCTACATCAGCCTCCTGCCCTGGCGATGGACTCACCTTGGCCTTAAGAT
CTAGGGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
CCTGAGTTAAATTGAAAATAAGTGGGGCTGGGACACAAAAAAA

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPWRGRREQCLLPPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDSSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGCAGCCGCTACGCCGCTGCAGCCGCTTCCGGCCCTGGGCCTCTGCCGTCA
 GC**ATGCC**ACACGCCCTCAAGCCC~~GGG~~ACTTGGTGGCTAAGATGAAGGGCTACCCTCAC
 TGGCCTGCCAGGATCGACGACATCGCGATGGCGCCGTGAAGCCCCAACCAACAAGTACCC
 CATCTTTCTTGGCACACAGAAACAGCCTTCCTGGGACCCAAGGACCTGTTCCCCTACG
 ACAAAATGTAAAGACAAGTACGGGAAGGCCAACAGAGGAAAGGCTCAATGAAGGGCTGTGG
 GAGATCCAGAACAAACCCCCACGCCAGCTACAGGCCCTCCGCCAGTGAGCTCCGCCAG
 CGAGGCCCCGAGGCCAACCCGCCAGGGCAGTGA~~C~~GCTGACGAGGACATGAGGACCGGG
 GGGTCATGGCGTCACAGCGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
 GACTCAGAACAGAGTAGCGACAA~~C~~AGTGGCCTGAAGAGGAAGACGCC~~T~~CGCTAAAGATGTC
 GGTCTCGAACAGAGGCCAACAGGCC~~T~~CCAGCAGCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCGACAGCAGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGCGCCACGGAGGGCCCTCTGGGGGGACGGAAAAAAAAGAA
 GGC~~CG~~CGTCAGCCTCCGACTCCAAGGCCATT~~C~~GGACGGGCCAAC~~C~~CTGAGCCGG
 TGGCCATGGCGCGGT~~C~~GGCTCCTCCTCCTCTTCCCTCCGACTCCGATGTG
 TCTGTGAAGAAC~~C~~CTCCGAGGGCAGGAAGCCAGCGAGAAGCCTCTCCGAAGCC~~G~~GAGG
 CGGGAAACC~~G~~AAGCCTGAACGCC~~T~~CCGTCCAGCTCAGCAGTGACAGTGACAGCAGGAGG
 TGGACCGCATCAGTGA~~G~~AGCAGGCCGGGACGAGGCCGGAGGCGAGCTGGAGGGCCCG
 CGGCGGGCAGAGCAGGAGGAGGAGCTGCCGCGCTGCCGAGCAGGAGAAGGAGGAGAAGGA
 GCGGAGGCGCAGCGGGCCACC~~G~~CGGGGAGGCTGAGC~~G~~GGGCCAGCGGGCAGCAGCGGGG
 ACGAGCTCAGGGAGGACGATGAGCCGTCAAGAACAGGGGGACGCAAGGGCCGGGCCGGG
 CCCCCGTCCTCTGACTCCGAGCCCAGGCCAGCTGGAGAGAGAGGCCAACAAATCAGC
 GAAGAACGCCAGTCCTCAAGCACAGAGCCCAGGAAACCTGCCAGAACGGAGAACAGAG
 TCGGGCCCGAGGAGAACAAACAAGCCAAGCCC~~G~~TGAAGGTGGAGC~~G~~GGACCCGGAACGGTCC
 GAGGGCTTCTGATGGACAGGAAGGTAGAGAACAGAACAGGCCCTCCGTGGAGGGAGAAGCT
 GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTGACAGGCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGAACCCCTGCAGGTGACCTCTCAGATCCTCCAGAAC
 ACAGACGTGGTG~~G~~CCACCTGAAGAACAGATTGCCGTACAAAGCGAACAAAGGACGTAATGGA
 GAAGGCAGCAGAACAGTCTATA~~CC~~GGCTCAAGTCGCCGGTCTCGGCCAACAGATCGAGGCCGG
 TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAACGCCAGGCCAGGAGAACAGCTGGCCGGGAG
 GAGCTGGCGGGGGAGGAGGCCAGGCCAGGAGAACGCCAGGCCAGGCCAGGCCAGGCCAG
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAACGGGGAGAGCGCAGAGGACAGGAGCACG
 AGGAGGGT~~C~~GGACTCGGAGGAGGGCCAAGGTGTGGCTCTGAAGAACCTGCACGACAGC
 GTACGGGAGGGT~~C~~CCGACCTGGACAGGCC~~T~~GGAGCAGGCCAGGCCAGGCCAGGCCAG
 GGGGGACTCGGAGGCC~~T~~GGACGAGGAGAGCT**TGA**GCCGCCAGGCCAGGCCAGGCCAGGCCAG
 CCGAGCTCAGGCTGCCCTCTCC~~T~~CCGCCGCTCGCAGGAGAGCAGAGCAGAGAAC~~T~~GTGGG
 GAACGCTGTGCT~~T~~TTGTATTGTC~~C~~CTGGTTTTTCTGCC~~T~~TAATTCTGTGATT
 TCCAACCAACATGAAATGACTATAACGGTTTTAATGA

FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPPIFFFTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGNEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDADEDDEDRG
VMAVTAVTATAASDRMESSDSDKSSDNSGLKRKTPALKMSVSKRARKASSLDQASVSPSE
EENSESSESEKTSQDFTPEKKAAVRAPRRGPLGGRKKKAPSASDSKADSDGAKPEPV
AMARSASSSSSSSSSDSVVKPPRGRKPAEKPLPKPRGRKPAPPERPPSSSSDSDEV
DRISEWKRDEARRRELEARRRREQEEELRRLREQEKEEKERRERADRGEAERGGSGGSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSACKPQSSSTE PARKPGQKEKRV
RPEEKQQAKPVKVERTRKSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNAL EELGT LQVTSQILQKNTDVVATLKKIRRYKANKDVM EKAAEVYTRLKSRLGP KIEAV
QKV NKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGE SAEDKEHE
EGRDSEEGPRCGSSED LHDSVREGPD LDRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA
 ACACCATTGAAAGAGAACATGTTTCATC**ATGA**ATGCTAATAAGATGAAAGACTAAAGCCAGAACCAAGA
 TTTTCACCTTTCTGCTTGATGATGCTAACGATGACCATGTTCTTCCAGTCAGTCACTGGCACTTTGAAGCA
 AAATATTCCAAGACTCAAGCTAACCTACAAAAGACTGCTGTTCAAATAGCTGTATTCCCTTTGGGTTCATC
 AGAAGGACTGGATTTCAAACTCTCTTAGATGAGGAAAGAGGCCAGGCTGCTTGGGAGCCAAAGACCAT
 CTTTCTACTCAGTCTGGTTGACTAAACAAAATTAAAGAAGATTATTGGCTGCTGCAAAGGAACGGGTGGA
 ATTATGTAATTAGCTGGGAAAGATGCAATACAGAATGTGCAATTTCATCAGAGTACTTCAGCCCTATAACAA
 AACTCACATATATGTGTGGAACGGAGCATTTCATCCAATATGTGGGTATTGATCTTGGAGTCTACAAGGA
 GGATATTATATTCAAACACTAGACACACATAATTGGAGTCTGGCAGACTGAAATGTCCTTCGATCCTCAGCAGCC
 TTTTGCTTCAGTAATGACAGATGAGTACCTCACTCTGGAACAGCTCTGATTTCTTGGCAAAGATACTGCATT
 CACTCGATCCCTGGGCTACTCATGACCAACTACATCAGAACTGACATTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTATTGAACTTCTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTTCTTCG
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTCTCGAGTTGGAGAGTTGTAAGAATGATGT
 AGGAGGACAACGCGCCGCTGATAAACAAAGTGGAGCAGCTTCTTAAGGCCAGACTGATTGCTCAATTCTGGAG
 TGATGGGGCAGATACTTACTTGATGAGCTTCAGAATATTATTACTCCCCACAAGAGATGAAAGAAATCTGT
 ACTATATGGAGTCTTACTACAACCAAGCTCCATCTCAAAGGCTCTGCTGTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTTAATGGTCCATATGCTCATAGGAAAGTGCAGACCATCGTGGGTGCACTGATGGGAGAAT
 TCCTTATCCACGGCCTGGTACATGCTCAAGGAAACCTATGACCCACTGATTAAGTCCACCGAGATTTCAGA
 TGATGTATCAGTTCTAAAGCGGCACTCTGTGATGATATAAGTCCGTATACCCAGTTCAGGAGGACCAACGTT
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCATTGCAAGAAGATGGCCAGTACGA
 TGTAATGTTCTTGAACAGACATTGGAACACTGCTCTCAAAGGTTGTCAGCATTCAAAGGAAAGTGGAAATATGGA
 AGAGGTAGTGTGGAGGAGTTGAGATATTCAAGCACTCATCAATCATCTGAACATGGAATTGTCCTGAAGCA
 GCAACAAATTGTACATTGGTCCCGAGATGGATTAGTCAGCTCTTGCACAGATGCGACACTATGGGAAAGC
 TTGCGCAGACTGTTGCTTGCAGAGACCCACTGTGCCCTGGGATGGAATGCATGCTCTGATATGCTCTAC
 TTCTAAAAGGAGAGCTAGACGCCAAGATGTAATGGCGACCAATCACCAGTGTGGGACATCGAAGACAG
 CATTAGTCATGAAACTGCTGATGAAAGGTGATTTGGCATTGAAATTAACTCAACCTTCTGGAATGTATACC
 TAAATCCAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGGATGAGCATGAGAGGAGTTGAGGCCGA
 TGAAAGAATCATCAAACGGAATATGGCTACTGATCGAAGTTGCAAGAAGAAGGATTCTGGGATGTTACTG
 CAAAGCCAGGAGCACACTTCATCCACACCAGTAGTGAAGCTGACTTGAATGTCATTGAGAATGAAAGATGGA
 AAATACCCAGAGGGCAGAGCATGAGGAGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAGA
 CTACATCCAATCCTTAGCAGGCCAAACTCAGCCTCGAGGACTGCAACAGATGTCACAGGGAGAAGCG
 GAGACAGAGAAACAAAGGGGGCCAAAGTGGAGCAGATGAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
 CAGAGACTGGATGAGCTTCTAGAGCTGAGCCACG**TAG**TTTCTACTTAATTAAAGAAAAGATTCTTAC
 TATAAAAACATTGCTTCTGTTGTATATCCCTATAGTAATCATAAATGTCCTCCATGGAGTTTGTCAAGG
 CACAAGACAATACTGAATAAGACAATATGTGATGAAATATAAGAAAGGGAAAAAATTGATGAAACCAGTTT
 CCAAGAACAAATCTGCACAAGCAAAAGTATAAGAATTATCCTAAAGGTTACAGTTGTAATGTTTA
 TGTTTGAGTTTGAATTATTGTATGAAATGAGCTAAGCAAGGCCAATTGATAGTGTATAAGGT
 GCTTTATCCCTCGAATGTCCTTAAGCATGGAATTACCATGCACTGCTATGTTCTATGAAACAGATATAT
 CATTCCTATTGAGAACAGCTACCTGTGGTAGGGATAAGAGGTGAGACACAAATTAAAGACAACCTCCATTATC
 AACAGGAACCTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTGGAGAGGTGCAATTCTTCTC
 TGGCCACTGGGTTAAATTAGTGTACTACAACATTGATTACTGAAGGGACTAATGTTCCCCAGGATTCT
 ATTGACTAGTCAGGAGTAACAGGGTACAGAGAGAAGTTGGTGTAGTTATGTGTTTTAGAGTATATACTAA
 GCTCTACAGGGACAGAATGCTTAATAATACCTTAATAAGATATGGAAAATATTTAATAAAACAGGAAAACA
 TAATGATGTATAATGCACTCTGATGGGAAGGCATGAGATGGGATTGTTAGAAGACAGAAGGAAAGACAGCCAT
 AAATTCTGGCTTGGGAAAACATATCCCCATGAAAGGAAGAACATCACAATAAAGTGGAGAGTAAATGTA
 TGGAGCTTTTCACTAGGGTAAAGTAGCTGCCAATTGTAATTGATCTGTTAAAGGAAATCTAGATTATAAC
 AACTGCTAGCAAAATCTGAGGAAACATAATTCTCTGAAAGAATCATAGGAAGAGTAGACATTATTATAACC
 AATGATATTTCAGTATATATTCTCTCTTTAAAAAAATTATTCATACTCTGTATATTCTTTTACTGC
 CTTTATTCTCTCTGTATATTGGATTGTTGATTATTTGAGTGAATAGGAGAAAACAATATATAACACACAGA
 GAATTAAAGAAAATGACATTCTGGGAGTGGGATATATATTGTTGAATAACAGAACAGAGTGTAAAATTAAAC
 AACGGAAAGGGTTAAATTAACTCTTGACATCTCACTCAACCTTCTCATTGCTGAGTTAATCTGTTGAATT
 GTAGTATTGTTTGTAAATTAAACAATAAAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPRLKLTYKDLLLSNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAHDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLSSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVVDYRLTQIVVDHVIaedGQYDVMFLGTDIGTVLKVVSIKEKWNMEEVVLEE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYKACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHEADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRRHRLDELPRAVAT
```

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTATCCTGGAGCATGCCACCAGCGGGGGAGCAGA
 CAACCTCCCAGGTAAAGCTGGGAGCAAGACCTGAAGCTGTTCTCAGGAGCCTGGTGTATTTCCCCCACCCAC
 CTCAGCAGTTCAGCCAGCAGGGACTGATCAGGTGTGTCCTGGAGTGGGAGCAGAAGGGCTGGCTGGCAAGA
 GTGGCCTGGAGAAAGAGGTTCAGCCTGACCAGCGAGCTGCCGTGACTACAAGATCCAGAACCATGGCATT
 GGGTGAGGTGGGGGGCACAGGTGTATGTCACCTCTTGACTCAGCAAGAAGAGCTGAGAGAGGGGATCTGG
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTTAAGGTAACAGTGTGGACAATAGTAA
 GAGCACAGTTTGAGGCTAGACGACATAGGTTCAAATTCTTCTGTTCTAGTTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACCTCTGGACTTCAATTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
 AGGGAAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAAGTCCCATACTAAGTCATGCC
 TATTTCCACCCACCCCTGTTCTGCCTTCCAACCAGGTACTGCAACAGACTGGAGCAGAGGCGGCAGGGCT
 CAGAGCAGGGAGGCTCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGCACAGGTGAGC
 AGGTGAAGGGGCTGCCGGCTGGCCCTGCTGCAGGGGCTGGCTAGATGTGGAGCGCTGGCTGAAGCCAGCA
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTC
 CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTTTGAGGAGCCTGCC
 CCCAAGCCCTGGCACAGGGGCCCTCCCTGCCCTGCACACGTGGTATTTGCTATCAGGCAGGGCTGAGGATG
 AGCTGACAATCACGGAGGGTGAATGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCG
 ACCAGCACGGAGGTAGGCTTGTCCCTGAGCGATATCTCAACTTCCCGACCTCTCCAGAGAGCAGCC
 AAGACAGTGACAATCCCTGCGGGCAGAGCCCACAGCATTCTGGCACAGGCCCTGTACAGTACACCGGACAGA
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGACTCATCCGCTGCTGCCCGGGCCCAAGATGGAGTAGATGACG
 GCTTCTGGAGGGAGAATTGGGGGGCTGTTGGGCTTCTCCCTGCTGGTGGAGAGGCTTGGGCCCC
 CAGGGCCACCTGAACTCTGACCCCTGAAACAGATGCTGCCGTCCTCTCCCTGCTGGTGGAGAGGCTTGGGCCCC
 CTACCTCTGTTGGATGGGCCCCCTGCACCTGCTGCCCTGGGACAAAGCCCTGGACTTCCCTGGGTTCTGG
 ACATGATGGCACCTGACTCAGGCCATGGTCCACACCTCCCCGCCGCTAAAGCCCGGATCTGGCACC
 CAGATCCCCCACCTGAAAGGCCAGGGAAAGCCTGACCCCCAGTGATGCTGTCCTATCTTCAAGCTGTCA
 CCACACCATCAATGATCCAGAGCAACACAGCAAAGCTGGAATGCCCTATTTCACCCCTCACCTCAAGGGT
 GGAAACTGCCCCTCCCATTCTAGAGCTGAAACCCACTCCTTTTCCATTGTTCTATCATCTCTAGGACC
 GGAACACTACCTCTCTCTGTCATGACCCATCTAGGTGGTGAATGCCGAAATCTCTGGGGCTGGAAACC
 ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTCCCCACCCCTGGCTCCATGACCCACCCACTCTGGATG
 CCAGGGTCACTGGGTTGGCTGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGGCCAGGATGCGAAGCAG
 CTGTAATGGCTGAGCGGATTATTGACAATGAATAAGGGCACGAGGCCAGGGCCTGGGCTTGTG
 CTAAGAGGGCAGGGGCCCTACGGTGCTATTGCTTAAAGGGCCACACGGCAGGGCAGGGCCTGCTCCAGCTGC
 GCTCATCATATGGAGCGAGGTGTTGGGAGGCGGGCAGGGCAGGGTGTGCAACTCAGGTGGAGTAGAGCTGG
 TGAGGGGCTGTGACCTCTCTGAGGGCCCCAGGCTGAGACTGTCACACTCAGGTGGAGTAGAGCTGGTCC
 AGCTGGGGGCTGGAGGAGACTTGGAGAAGGGAAACAATACACTGTTCTGTCAGCTGGTAG
 TCCATCAGCACAAATGAAGGAGACTTGGAGAAGGGAAACAATACACTGTTCTGTCAGCTGGTAG
 TTTTCCCTGGGCTCCAGGACCTTCCCTACCTCCACCAACCAAGGGATTATAGCAAAGGCTAAGCCTGC
 AGTTTACTCTGGGGGTTCAAGGAGCCGAAAGGTTAAATAGTTAAGTAGGTGATGGGAAGATGAGATTACCTCA
 TTTAGGGCTCAGGAGACTCACATACTCCCTGCTCCCTGTTAGAGACACCTGAGAGAAAGGGAGGG
 TCAACAATGAGAGACCAGGGTAGGTCTATCAGTCCCCCAGAGTAGAGAGCAATAAGAGCCAGGCCAGTGC
 AGTCCCAGGCTGTGTTCTCACCTGGTGATCAGAAGTGTCTGGTTGCTGGCTGCCATTGCTTGGAGTAG
 GCAGCCCTGGCTGGGCCCTCCCTCCGGCCCTCAGTGTTGGCTTGCAAGGCTGGGGTTCCCTCAAGTG
 CACGAGGGGTTAGGTGCTGTCCTGAGTCTCCATTCTGTAAGGGGGCTGGCTAGGACCTGGGGCTGTGG
 TCTCAGGGGGCAGCCTCTCATGGCAGGCATCCCTGCCCTGGGCTGCCCTCCCCAGACCCCTGACCACCC
 GGTCTGCCCCCACCAGAGGCCAGCTCTGCTGTTGGGGAGCCATCACGGTGTCTGCAAGTCCATAGCG
 TCTCAATGTGTCTACCCGGAACCTGGAGGGGAGGGAAACACTGGGGTTAGGACCAACTCAGAGGCTG
 GCCCTCCCTCTGACCAAGGGACATCTGAGTTGGTGGCTACTCCCTCTGGCTTAAGGTAGGGGAGGC
 AGATTTGGGGGACATTGTTGAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCAAGGCC
 TTGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGGCCCCCTTCCCTGGAGCAGCTGCCCA
 CAGAGAACACAGTGGTCTCCCTGTCGGGGGGGGCTGAGAGGCCAGGTGCACTGTTGAGTAGGG
 GCCTCTGCTGCGGCTGCAATGGATGCAAGGGGCTGAGAGGCCAGGTGCACTGTTGAGTAGGG
 CGTCTGCAAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGGAGGTGAGGGTAACATT
 TCATGTTTGTCTTACGTTCTTCAAGCATGCTCTTAAAACCCAGAACGCCAATT
 TTTCTTGCTTTATCTAATAACTCAATATTAG

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLOEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESSQDSNDNPGCAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRGVFVPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVILPGDKALDFPGFLDMMAPRLRPMRPPPPPAKAPDPGHPDPLT
```

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FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAGAGAGACAGAGACAAAGGCACAGCGGAA
 GAAGGCAGAGACAGGGCAGGCACAGAACGGCCCAGACAGAGTCTACAGAGGGAGAGGCCAGAGAACGCTGCAGA
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAGGAGGGCTCAGGAGGAGATTGGAGAACGCCAGACCCCTGG
 GCACCTCTCCAAGCCAAGGACTAAGTTTCTCCATTCTTAACGGTCTCAGCCCTCTGAAAACCTTGCC
 TCTGACCTTGCGAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGTTCAAAGCTAGGGTGTGGAGGACTTGG
 GCCCTAGACGGCCTCAGTCCCTCCAGTGCAGTACCGATGCAATGTCCCAGACAGGCTCGCATCCGGAGGG
 CTTGGCAGGGCGTGGCTGTGGGAGGCCAACCCCTGCCCTCTGCTCCCATTTGTGCCCTCTCCTGGCTGGTGTG
 GCTGCTTCTGCTACTGCTGCCCTCTCTGCCCTCAGCCGGTGGCCAGCCCCCTCCCCGGAGGAGGAGAT
 CGTGTTCAGAGAACGCTCAACGGCAGCGCTGCCCTGGCTGGCGCCCTGCCAGGCTGTTGTGCCGCTTGCA
 GCCCTTGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCAGGGCTGACACTGCAGTA
 CCTGGGCCAGGCGCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTGCACGGGATGGGGAGCCCTGTTAGGCGTGTACAATATCGGGGGCTGAACCTCA
 CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACACTGCTGGGGACCTGGGCTCACATCCTACGCCGAAGAGCTC
 TGCCAGCGTCAAGGCTCCATGTCAACGTCAGGCTCTTGAAGCCCCAGCCCCAGACCCGAAGAGCCAA
 GCGTTTGTCTCACTGAGTAGATTGTGGAGACACTGGTGTGGCAGATGACAAGATGGCGCATCCACGGTGC
 GGGGCTAAAGCGCTACCTGCTAACAGTGTGGCAGCAGCAGGCCCTCAAGCACCAAGCATTCCGCAATCC
 TGTCAGCTTGTGGTGAECTCGGCTAGTGTACCTGGGTCAGGGCAGGAGGGCCCAAGTGGGGCCAGTGTGC
 CCAGACCCCTGCGCAGCTCTGCGCTGGCACGGGGCCCTAACACCCCTGAGGACTCAGGGCCCTGACCAATTG
 CACAGCCATTCTGTTACCGCTCAGGACCTGTGATGGCTCCACTGCGACACGCTGGTATGGCTGATGTGG
 CACCGCTGTGACCCGGCTGGAGCTGCCCCATTGTGGAGGATGATGGCTCCAGTCAGCCTTCACTGCTGCTCA
 TGAACGGTCTGTTCAACATGCTCCATGACAACCTCAACGGCATGATGGCTCATGGGCTTGAATGGGCTTGG
 CTCTCGCAGTGTGATGGCCCTGTGATGGCTCATGGGACTCCTGAGGAGCCCTGGTCCCCCTGCAGTGCCTG
 CATCACTGACTTCTGGACAATGGCTATGGCACTGTCTTAGACAAACCAGAGGCTCCATTGCACTGCTG
 GACTTCCCTGGCAAGGACTATGATGCTGACGCCAGTGCAGCTGACCTTGGGCCACTCACGCCATTGTCC
 ACAGCTGCCGCCGCTGTGCTGCCCTGTTGCTCTGGCACCTCAATGCCATGCCATGTGCCAGACCAAACA
 CTCGCCCTGGCCGATGGCACACCCCTGCCGGCCACAGGCCATGGGCTGCCATGGGCTGCCACATGGACCA
 GCTCCAGGACTTCATATTCCACAGGCTGGCTGGCTGGGCTCTGGGACCATGGGACTGCTCTGGGACCTG
 TGGGGTGGTGTCCAGTTCTCTCCGAGACTGCACGGCTGTCCCCCGGAAATGGTGGCAAGTACTGTGAGGG
 CCGCGTACCGCTCCGCTCGAACACTGAGGACTGCCAAGTGGCTCAGCCCTGACCTTCCGGAGGAGCA
 GTGTGCTGCCCTACAAACCCACCGCACCTCTCAAGAGCTCCAGGGCCATGGACTGGGTTCTCGCTACAC
 AGGGTGGCCCCCAGGACCACTCACCTGCCAGGCCGGGACTGGCTACTACTATGTGCTGGAGCC
 ACGGGTGGTAGATGGGACCCCTGTCGGGAGGCTGCTGGGAGGGGAGGGTCTGGTTGCAG
 CTGTGATGCCATATTGGCTCAAAGAAGATTGACAAGTGTGATGGTGTGCGGAGGGGAGGGTCTGGTTGCAG
 CAAGCAGTCAGGCTCTCAGGAAATTCAAGTACGGTACGGATAACAACATGTGGTCACTATCCC
 CGGGGGGACCCCA
 CATTCTTGTCCGGCAGCAGGGAAACCCCTGGCACCGGAGCATCTACTTGGGCTGAAGCTGCCAGATGGCTCTA
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGAGTCAGCTTG
 CAGCGGGGCCACTGCAGCCTCAGAGACACTGTCAGGCCATGGGCACTGGCCAGCCTTGACACTGCAAGT
 CCT
 AGTGGCTGGCAACCCCCAGGACACACGCCCTCGATACAGCTTCTCGTGCCTGGGGGACCCCTCAACGCC
 CCCCCACTCCCCAGGACTGGCTGCCAGAACAGACAGATTCTGGAGATCCTCGGCCGGGCCCCCTGGG
 GAGCAAATAACCTCACTATCCGGTGCCTTCTGGCACCGGGCTCGGACTTAGCTGGAGAAAGAGAGAGCTT
 CTGTTGCTGCCCTAGCTAACACTCAGTGGGAGGGCTGTGGCTGAGACCTGCCCTCTCTGCCCTAAT
 GCGCAGGCTGCCCTGCCCTGGTTCTGCCCTGGAGGAGTGTGGTTAGTGGATGGAAGGGCTGACAGAC
 AGCCCTCATCTAAACTGCCCTCTGCCCTGCCCTGGGTACAGGAGGGAGGGGAAGGCAGGGAGGGCTGG
 CAGTTGTATTATTAGTATTACTTACTTTATTAGCACCAAGGGAAAGGACTAGGGCTGGTGTAGGTATAAG
 TGGTGTGCTGCCCTAGCCCTCACGCCCTGCCCTGGGGCTAGGAAATCCAGGGCTGGTGTAGGTATAAG
 TGGTGTGCTGCCCTAGCTAACACTCAGTGGGAGGGCTGTGGCTGAGACCTGCCCTCTCTGCCCTAAT
 TTCTGTAATTATTATTGGAAAAGAAAAGTCAGGGTAGGGTGGCTCAGGGAGTGGGATTATCTTT
 TTTTTTTCT
 GCACAACTCTGGCTCACTGCATCCTCCGCTCCGGGTTCAAGTGTATTCTCATGCCCTAGCCCT
 GGATTACAGGCTGCCACGCCAGCTAACATTGTTGTTGTTGGAGACAGAGTCTCGCTATTGTC
 ACCAGGGCTGGAAATGATTCAGCTCACTGCAACCTGCCACCTGGGTTCCAGCAATTCTGCC
 CGAGTAGCTGAGATTAGGCACCTACCAACGCCGGCTAACATTGTTGTTAGTAGAGACGGGTTTCAC
 CATGTTGCCAGGCTGGCTCGAACCTCTGACCTTAGGTGATCCACTGCCCTCATCTCC
 AAAGTGTGCTGGGATTACAGG
 ACAGGCAGTGGCCACCGTGCCTGGCACGCCAACTAATTGTTGTTAGTAGAGACAGGGTT
 CACCATGTTGGAGTCAGACAG
 TGGCCAGGCTGCTCTGAACTCCTGACCTCAGGTAATCGACCTGCCCTGCCCTCC
 AAAGTGTGCTGGGATTACAGG
 TGTGAGCCACCACGCCGGTACATATTAAATTGAATTCTACTATTATGTGATCCTTGGAGTCAGACAG

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTCTCATTTGCCAATAATAATACCTCCCTTAGAAG
TTTGTGAGGATTAATAATGTAATAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGGAAA
AAAAAAAAAAAAAAAAGGAAA

FIGURE 180

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVLPGSGAPARLLCRLQAFGETLLEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTGTINGDPESVASLHWGGALLGVLQYRGAEHLHQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVVTRLVIIGSGEEGPQVGPSAAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
NSKPCISLNGPLSTSRRVMAPVMAHVDPPEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PTVTPGKDYDADRCQLTFGPDSRHPQLPPPACAALWCSGHINGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRVPVRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMWDWPRYTGVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVTI PAGATHILVRQQGNPGHSRISIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRPWAGRK
```

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
 CAAAGAACCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCC
 AAGAAAATATGTAAATCACTTAAGATTGTGGACTGGTGGTATCCTGGCCCTAACTCT
 AATTGTCCTGTTGGGGAGCAAGCACTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGATTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTCAAGAGCGGAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACTGGCATCTACTCGTGGTCTCAAAAATGTTTATCAAAACTCAGA
 TTAAAGTGATTCTGAATTTCTGAACCAGAAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACATTCTTGAAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTCTTAAAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTCTGAGTTACAAGACTTGGGAGGGAGAAGATCTCACCTT
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGAAGAACCTCCAATAAATGACTATACTG
 AAAATGGAATAGAATTGATCCCAGTGGATGAGAGAGGTATTGTGTATTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCCGTCTGTGAACCTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACCGAGTCATCTGTCGTGTACATGCCCTGTAAGTGGTGGTGGCCC
 GCATGCTGGGAGGGTCTAAAGGAGGTTGAGCTCAAATGCTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCCAGAATTACTGTAGGTAATTCTCTTCATGTTCTAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLIVLFWGSKHFVPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEETTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPAKEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMELDERGYCCIYCRRGNRYCRRVCEPLLGYYPPYCYQGGRVICRVIMPCNWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGCGTGACCCCCAGGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTCTGGGCTTCCT
 GCTCAGCTTCCCTGGGCATGGTGGCACGTTGATCACCAACATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGCACCAACATCCTCACGGCGTGTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCGCCTCATGGTCATCTCCTGCCCTCTCGGGCATAGCCT
 GCGCCTGCCGTATCGGGATGAAGTGCACGCGCTGCCAACAGGGCACACCCGCCAAGACC
 ACCTTGCCATCCTCGGCGCACCCCTTCATCCTGCCGCCCTGTGCATGGTGGCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCCAGCGGCATGA
 AGTTTGAGATTGCCAGGCCCTGTACCTGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCCCTGCTTGCCTGTCCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCGCC
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCCTACAGGCCACCAGCTGCCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTCTCCCTGGCTGCTGTGGCTGGGTCCCCGGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTACTTCTGGCAATTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTAGAGACAGGGACAGAGGGGAAATAAGAGGGAGGAGAA
 AGCTCTCTACCAAAGACTGAAAAAAAATCCTGTCTGTTTGATTTATTATATATAT
 TTATGTGGGTGATTTGATAACAAGTTAATATAAGTGACTTGGAGTTGGTCAGTGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCAGGATGTGGCTGTTATGAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGLTITLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAWSWTNDVQNFYNPLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCTCAGGAGCGCGTTAGCTTCACACCTCGGCAGCAGGAGGGCGGCAGCTCTCG
 CAGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACATGCCAAGTGGTGGCGTTCC
 CCTGTCCATCCTGGGCTGGCGCTGCATCGCGCCACGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCATTTCACCATCCTGGACTTCCAGC
 CATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGCCTGGGTGCCATTGCCCTCC
 TGGTATCCATCTTGCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGATCATGTTCATTGTCTCAGGTCTTGCAATTGCTGGAGT
 GTCTGTGTTGCCAACATGCTGGTACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGCAGGCTCTGTTCTG
 GGCTGGGTCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGG
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTCTTATCATGCCCTCAGGCCACAGTGGT
 CCTACAAAGCCTGGAGGCTCAAGGCCAGCAGGCTTGGCTTGGTCCAACACAAAAACAAGAAG
 ATATAACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAACGACTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTCACCCAAA
 AACAAAGGAGATCCCATCTAGATTCTTCTGCTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTCATCTTGGAGAGGCCAAATGGCTTAGCCTCAGTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCATCCTCTAT
 TTCTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTAATCTCTCTCAC
 ATTGATGATTAGACAGACTCCCCCTCTCCTCTAGTCATAAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCCAAGAAAACCTTGAAGGAAAGAGTAGACCCAAAGATGTTATT
 CTGCTGTTGAATTTGCTCCCCACCCCAACTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTGTAATCTCTCCAGCCCATGATCTGGTTTCTTACACTG
 TGATCTAAAGTTACCAAACCAAAGTCATTTCAGTTGAGGCAACCAACCTTCTACTG
 CTGTTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG
 TCCTCTTCTGCGGGTCAGAAATTGCTCTAGATGAATGAGAAAATTATTTTTAAT
 TTAAGTCCTAAATATAGTAAATAAATAATGTTAGTAAATGATACTATCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGTCT
 ATATGGTACTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCATGGT
 GCATACACCTGTAGTCCAGCATTCCGGGAGGCTGAGGTGGAGGATCACTTGAGCCCAGGG
 AGGTTGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
 ACTAATTCTTAA

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSFVANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYP SKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAAACTGTTCTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATA**ATGG**CAACCCATGCCTTAGAAATCGCTG
 GGCTGTTCTGGTGGTGGATGGTGGGCACAGTGGCTGTCAGTGTGATGCCTCAGTGG
 AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTCTCGGACCTACAGGCAGGCCAGAGGACTGATGTGCTGCTCCGTGATGTCCTTC
 TTGGCTTCATGATGGCCATCCTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCATCACGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT
 GTTGCCCAAAACGTGAGCTGGAGAACGCTCTACTTAGGATGGACCA CGGC ACTGGT GCT
 GATTGTTGGAGGAGCTGTTCTGCTGCCTTTGTTGCAACGAAAAGAGCAGTAGCTACAG
 GATACTCGATACTTCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTATGTTTAACTTACTATAAACG
 CATGCAAATGACAAAAATCTATATTACTTCTAAAATGGACCCCAAAGAAACTTGATT
 CTGTTCTTAACTGCCTAATCTAATTACAGGAACGTGCATCAGCTATTGATTCTATAA
 GCTATTTCAGCAGAATGAGATATAAACCCAATGCTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTCTAAGGTGGTTCAAGCATCTACTCTTTATCATTACTTCAAAATGACATTGCT
 AAAGACTGCATTATTTACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTATCTCACATAGAGACATGCTTATATGGTTATTAAAATGAAATGCCAG
 TCCATTACACTGAATAAAATAGAACTCAACTATTGCTTTCAGGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAAATTGTTAAAACAGCTTAGGGATTAATGTCCTCCATTATAATGA
 AGATTAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG
 TTTTTAGCCTAGGAGTTAGAAATCCTAACCTTCTTATCCTCTCCAGAGGCTTTTT
 TTCTTGTATTAACATTAAACATTAAACGCAGATATTGTCAGGGCTTGCATTCA
 AACTGCTTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTG
 GTTTAGGAAAGTGAATAATTTGTTTGTATTGAAGAAGAATGATGCATTGACAA
 GAAATCATATATGTATGGATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATC
 AATATAAATAAAAGAGCAGAAAAATATGCTTGGTTTCTTACCAAAAAACAAACA
 ACAAAAAAAAGTGTCTTGAGAACCTCACCTGCTCTATGTGGGTACCTGAGTCAAAATTG
 TCATTCTTGTGAAAAATAAATTCTTCTGTTTATCCTGTTGACCTTCTGTTAGTTACTAAA
 ATCTGTAATACTGTATTTCTGTTATCCTGAAACTGACAATCCAATTG
 AAGTTGTGTCGACGTCTGCTAGCTAAATGAATGTGTTCTATTGCTTATACATTATA
 TTAATAAATTGTACATTCTAATT

FIGURE 188

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPIVSVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**ATGG**CCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAAGGTGACCGCTTCATCGGCAACAGCAT
 CGTGGTGGCCCAGGTGGTGGGAGGGCCTGTGGATGTCTGCCTGGTGCAGAGCACCGGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTACGCCCTCCTGTGGCCTGTTGGCTGCTGGTCTACCTGCTGGGC
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCACCTCTGGGA
 TTGTCTTGTCATCTCAGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGATGCCATC
 ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCAAAAGCGGGAGCTGGGGCCTCCCT
 CTACTTGGCTGGCGCCCTCAGGCCTTTGTTGCTGGGTGGGGTTGCTGTGCTGCACCT
 GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGCCCGCTACTCAACATCTGCCCT
 GCCATCTCTCGGGGGCCCTCTGAGTACCCCTACCAAGAATTACGTC**TGA**CGTGGAGGGAAATG
 GGGGCTCCGCTGGCGCTAGGCCATCCAGAAGTGGCAGTGCCAACAGCTTGGATGGTT
 CGTACCTTTGTTCTGCCCTCTGCTATTCTTGACTGAGGATATTAAAATTCACTT
 GAAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTCTCACCTTGG
 ATGATGGAGCCAAGAGGGATGTTGAGATTCTGGATCTGACATGCCATCTAGAAGC
 CAGTCAAGCTATGGAACTAATGCCAGGCTGCTTGCTGGCTTGCAACAAAGACAGAC
 TGTCCTCAAGAGTCTGCTGCTGCTGGGGCTGGCTTCCCTAGATGTCAGGGACAGCTG
 CCCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTTACCCCTGGAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCCGAACTTCTGACCTCTGTTCTCCGTCTGATAAGACG
 TCCACCCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCAAACACTGCACC
 CTTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAGCATG
 TTTTGTAGTGCA

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWNVNGLVSCALPMWKVTAFIGNSIIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSIV
FVISGVTLIIPVCWTAAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLLCTCP
SGGSQGPSHYMARYSTSAPAISRGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTCTAGACTCAAAAGGCTTCCACGTTACATCTTG
 AGCATCTTCTACCACCTCGAATTGAACCAGTCTCAAAGTAAGGCATGGCATTATCCC
 TTGCAAATTGCTGGGCTGGTCTGGGTCCTGGCATGGTGGGACTCTGCCACAACCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTGTTGGCAGCAACATTATTGTCTTGAGAGGCTC
 TGGGAAGGGCTCTGG**ATG**AATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGCTCCTTGTGGCTCCCCGCTGCCCTGGAAACAGCCGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTGATGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGCAAAGCATACTTCTGGGAACCTCAGGAGTCCCTCATCCTGAC
 GGGTATCTTGGTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
 ACCCAGCCATCCACATAGGTCAAGAACGAGAGCTGGGAGCAGCACTTTCTGGCTGGCA
 AGCGCTGCTGTCCTCTCATGGAGGGGCTGCTTGTGGATTTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCACCAGTTATGTC**TAA**TGCCTCTTGGCTCCAAGT
 ATGGACTATGGTCAATTTTATAAGTCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
 GAACTTGCTTATGTCTAGATTACATTGATAACGAAAGTTCAATTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
 GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATAACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAAATTGATATTCTATAACAATAAACATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKVQCTGSNER
AKAYLLGTSGVLFILTGIFVLI PVSWTANIIIRD FYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRKKQGYRYPVGYRVPTDKRRNTMLSKTSTS YV
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGC**ATGA**AAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCATCA
CATACCTACCAGTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTCTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAAGAGTAATCTG
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTAACACGTCAATAAAAAATAATCTCCCAGA

FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNDRVQFLHDGSC
```

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCCGGTTCTCCCTCGCAGCACCTCGAAGTGC
GCCCTCGCCCTGCTGCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGCCCAGGTGGCATAAGTGGAAATAA
ACTCAAGCTGATGCTCAA
AACGAGAAGCACCTGTTCCA
ACTAAGACTAAAGTGGCGTTGATGAGAATAAGCAA
AGATTCCCTGGCAGCCTGAAGGCCAGAAGCGGCAGCTGTGG
ACGGACTCGGCCGAGGTGC
AGCAGTGGTACCA
CAGCAGTTCTACATGGC
TTGATGAAGCGAAATT
GAAGATGACATC
ACCTATTGGCTTA
ACAGAGATCGAA
ATGGACATGA
AAACTATGGC
GATTACTACCA
ACGTCA
CTATGATGAAG
ACTCTGCA
ATTGGTCCCCGG
AGCCCTACGG
CTTAGGC
ATGGAGCC
AGCG
TCAACTACG
ATGACTAC
TAA
CCATGACTTG
GCCACACG
CTGTACA
AGAAGCAA
ATAGCG
ATT
TCTTC
CATGTATCT
CCTAATGC
CTTACACT
ACTTGG
TTCTG
ATTTG
CTCTATT
TCAGC
AGAT
CTTTCT
ACCTACTT
GTGTGAT
AAAAAGA
AGAGTT
AAAACA
CACATG
TAAATGC
CTTT
TGATATT
TCATGG
GAATGC
CTCTC
ATT
AAAAAT
AGAAATA
AGCATT
TTGTT
AAAAGA

FIGURE 196

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLCWGPGGISGNKLKMLQKREAPVPTKTKAVVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNRDRNGHEYYGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY
```

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCGCCGGAAAGTCCCCGAGGGGCCGATGGAGCTGGGGAGCCGGCGCTC
 GGTAGCGCGGGCAAGGCAGGCATGACCTGATTGAAGGGTGGGTATGAGGTGAC
 CGTCCTTTCTCGGTGCTTGCTGCCTCTGGTGCTGGCCCTGCCTGGTCTAACGCACA
 CCGCTGAGGGCGGGACCCACTGCCCAAGCCGTAGGGACCCAACGCCATCCCAGCCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGTTACAGCAACACCGCCAG
 CCCCGGACTCCCCGAGGAGCCCTCGTGTACGGCTGAAATTCCCTAATGATTAGCAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTGAAAAGGACCCAGTTCCCGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
 GCAGCCTTCACCTCCCTCCAACTGCCTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAAATCCCCCTGCCGCCGGGTCCGAGCCCGGCCCTCCGGCTGGAAATCGGCAGCCT
 GCTGCTGCCCTGCTGCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGC
 CCTCTTCCCTGACGCCACTCTGGCCTGGCCGCTTCACCCTGCTCCTCAGTCTCCTG
 GCCTTGCCATGTACCGCCTAGGCCTCCGCCGGCGCTGGCAGCGTCGCCGGCCCTCC
 GGACCTTGCTCCCCGCCGGCGCTGGAGGCCAGCCCTGCCAGAGGACTCCCGGACTGGCGGAGG
 CCTCTCCGCTGCCCTGGAGGCCAGCCCTGCCAGAGGACTCCCGGACTGGCGGAGG
 CCCGCCCTGCGACCGCCGGGCTCGGGCACCTCCGGGCTGCTGAACCTCAGCCCGCA
 CTGGGAGTGGGCTCCTCGGGCATCTGCTGCTGCCCTGCCGGCCAGAGCCG
 GGCGCCCCCGGGGCCGTCTAGTGTCTGCCGGAGGACCCAGCCCTCCAATCCCTGAC
 AGCTCCTGGGCTGAGTTGGGACGCCAGGTGGTGGAGGCTGGTAAGGGAGCGGGAG
 GGGCAGAGGAGTTCCCCGAACCGTGCAGATTAAAGTAACGTGAAGTTAAAAAAA
 AAAAAAAA

FIGURE 198

MTLIEVGVDDEVTLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLGLAGFTLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCCCTCCAAGG**ATG**ACAAAGGCGCTACTCATCTATTGGTCAGCAGC
TTTCTTGCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG
AAAGCAAGTTAACATATCAAAGATAAAATGAAAATGCGGATGGAAGCTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCAACCTTCTGCAGGCATCCACTGCGAAAAAGGA
TTGTGTCCGGAGCACGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTCAAGGCCGG
CCACTCTCCTACTGGTGACAGGATGCCGCTGAGA**TGA**ACAGGGTGCAGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTCTTCTTCACTGCCTCCA
CTTCATGTTATTTCTTCCCTCCATTACAACAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTCTTGGCTTCCCTACTCCCCTGACCCAGTCCCCTGGTTCTGTCTGTAT
TTGTAAACTGAGGACCACAATAAGAAATCTTATATTATCG

FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSSENLCVDCQDLLNPNLLAGIHCRAKRIVGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18

4 10 16 22 28 34 40 46 52 58 64 70 76 82 88 94 100

FIGURE 201

TCTGACCTGACTGGAAAGCGTCCAAAGAGGGACGGCTGTAGCCCTGCTTGACTGAGAACCCA
CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGAAAGAAACACCTGAG
CAGAATGGAATCATTATTTTCCAAGGAGAAAACCGGGTAAAGGGAGGGAAAGCAATT
AATTGAGTCCTGTGAATGGGCTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
TTGGGTGAAACTGGGTCTGTGGTTCTGATTGTAAGTGAAGCAGGTCTGCACACGC
TGTTGCCAAATGTCAGGACCAGGTTAAGTGAAGCAGAAAAACTCCAGGTGAAACAAGCA
ACCCATGTTCTGCTGCAAGCTGAAGGAGCCTGGAGCAGGGAGAAAGCTAAGTGAACATGAC
CTGTTGCATTGGCAAGTTCTAGCAACATGCTCTAAGGAAGCGATAAGGCACAGACCATG
CAGACTCCAGTTCCCTGCTGCTCCTGATGCTGGATGCGTCCTGATGATGGTGGCGATG
TGCACCCCTCCCCACCACACCCTGACAGACTGTACAGCCCAAGGCCAGCAAGCACAGCC
GAAGCCAGGTACCGCCTGGACTTGGGAATCCCAGGATTGGTACTGGAAGCTGAGGATGA
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCCTTATCTCACTGCGGGAGGATCAGC
TGCTGGTGGCCGTGGCCTTACCCCAGGCCAGAAGGAACCAGAGGCCAGGGCAGGAGAGGTGG
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
GGCTGATGAGGACGGGGAGGTGCTGAAGAAAGAGGAGTTGACCCGTTCAGCCTGGACCCAC
GTGGCCTCCAGGAGGCACTCAGTGCCGCATCCCCCTCCAGAGGGCTTGCCCGAGGTGCGG
CACCCACTGTGTCTGCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
TTTCCATGATGAGGCCTGGTCCACTCTCCTGGGACTGTACACAGCATCCTGACACAGTGC
CCAGGGCCTTCTGAAGGAGATCATCCTCGTGACGACCTCAGCCAGCAAGGACAACCTCAAG
TCTGCTCTCAGCGAATATGTGGCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
GCTGGGTGCCATCAGGGCCGGATGCTGGGGCCACCAGAGCCACCAGGGGATGTGCTCGTCT
TCATGGATGCCACTGCGAGTGCCACCCAGGCTGGCTGGAGGCCCTCCTCAGCAGAAATAGCT
GGTGCAGGAGGCCAGTGGTATCTCCGGTGTAGATGTGATTGACTGGAAGACTTCCAGTA
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTCCACTGGGAAC
CTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG
GTGCCCGAGAGGTGGGCCATGGACAGACATTACTTCAAAACACTGGAGCGTATGACTC
TCTTATGTCGCTGCGAGGTGGTAAAACCTCGAACACTGTCTTCAAGGCCCTGGCTCTGTGGTG
GCTCTGTTGAAATCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCCAT
TCCCCCTCGACCAGGAGGCCACCCCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGG
GTCATTCAAAGAAACCTTCTACAAAGCATAGCCCAGAGGCCCTCTCCTTGAGCAAGGCTGAGA
AGCCAGACTGCATGGAACGCTGCAAGGAGACTGGGTGTCGGACATTCCACTGG
TTTCTGGCTAATGTCTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTCTCTGGAAA
GCTCCACAACACTGGACTTGGCTCTGTGCAGACTGCCAGGCCAGAAGGGGACATCCTGGGCT
GTCCCATGGTGTGGCTCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
AGGAAGGAGATTCACTTGGCAGGCCACAGCACCTGTGCTTTGCTGTCAGGCAGGAGCAGGT
GATTCTCAGAACTGCACGGAGGAAGGCCTGGCATCCACCCAGCAGCACTGGGACTTCCAGG
AGAATGGGATGATTGTCACATTCTTCTGGAAATGCATGGAAGCTGTGGTGAAGAAAAC
AATAAGATTGTACCTGCGTCCGTGTGATGGAAAAGGCCGCCAGCAGTGGCGATTGACCA
GATAATGCTGTGGATGAACGATGAATGTCAATGTCAAGGAAAAGAGAATTGGCCATC
AAAATCCAGCTCAAGTGAACGTAAGAGCTTATATATTTCATGAAGCTGATCCTTTGTGT
GTGTGCTCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTCTCCTT
TCACACCTTATTCACTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLMLGCVLMVAMLHPPHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFOYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIFYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEPDCMERLQLQRRLGCRTFWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQQVILQNCTEEGLAIHQHQHWDQENGMIHVILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFQDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**
 GTCCAGGATGTGGCCTGCGCTGCTGCTGCCACCTCCTCCCTCTGGCCACTGCTGTTGC
 TGCCCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCCTCGAACCCCACCAGCCCCAGCC
 CGCCCCCCCCTGTGCCAGGGGAGGCCCTGGCCCCACGTCATGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGGCAAGTCCTGCCTGGCACTG
 CACCCCCAGCCACCCATCAGGCTTGGAGGGGCCGCCATCCCAATACCCCTGGGCT
 ATCGTGTGGGTCCCACCGTGTCTCGAGAGGATGGAGGGACCCAACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTGAGCCCCCTCATGGGCTCGCAACCCCACACCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTGGAGAGGCACCTGCCACCCCTGCGGCCATT
 CTGTTGGGGGGCGTGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT
 CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAGTTCTGCTGGGACCGCAGCCAGAAC
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGAGGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGCCTCGGGACTCACCTACCCCCACCCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGCTGGGATGCCCAACCCAAAGGGGCTCCAG
 CCTTCCAGTTGAACCGG**TGA**GGGCAGGGCAATGGGATGGGAGGGCAAAGAGGGAAAGGCAAC
 TTAGGTCTTCAGAGCTGGGGTGGGGTGCCTCTGGATGGTAGTGAGGAGGCAGGCGTGGC
 CTCCCCACAGCCCTGGCCCTCCAAAGGGGCTGGACAGCTCCTCTGGAGGGCACCCTTC
 CTTCTCCAGTCTCTCAGGATCTGTGTCCTATTCTCTGCTGCCATAACTCCAACCTGCC
 TCTTGGTTTTCTCATGCCACCTGTCTAACACAACCTGCCCTCTAACCTGATTCCC
 CCTCTTGCTTGAACCTCCCTCTATTCTGCCCTACCCCTGGTTCTGACTGTGCCCT
 TCCCTCTCCTCTCAGGATTCCCTGGTAATCTGTGATGCCCAATGTTGGGTGCAGCC
 AAGCAGGAGGCCAAGGGCCGGCACAGCCCCCATCCACTGAGGGTGGGCAGCTGTGGGA
 GCTGGGGCCACAGGGCTCCTGGCTCCTGCCCTTGACACACCACCGGAACACTCCCCAGCC
 CCACGGGCAATCTATCTGCTGCCCTCTGCAGGTGGGGCCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTCAC
 AGGCCATTGACACGCTCTGCACCCCTCTCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCGTCTCACATTGCACTCTCCTCTCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTCTGCACACTTACCTCTCATGTGCGTTCGGGCTGATGTTGTGGTGG
 TGTGCGGCGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTCCGCAGCCCTGC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGCTCCTGGGCCCTCATCGGTATGG
 TCTCGTCCCATTCCACACCATTGTTCTGTCCTCCCATCCTACTCCAAGGATGCCGGCA
 TCACCCCTGAGGGCTCCCCCTGGGAATGGGTAGTGAGGCCAGACTCACCCCCAGCCCA
 CTGCTAAAATCTGTTCTGACAGATGGGTTGGGGAGTCGCCTGCTGCACTACATGAGAA
 AGGGACTCCCATTGCCCTCCCTTCTCCTACAGTCCCTTGTCTTGCTCTGCTGGCTG
 TCTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTCCAGCCT
 CCCTTGGGCCTCCCTAACCTCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTCAAGGCC
 ATCGGGAGCTGCTGCCCTCAAGTCTACCCCTCCCTCCGGACTCCCTCCTGTCCCTCCTT
 CCTCCCTCCTCCCTCACCTCTCCCTTGTCTCCCTGCCCTTCCCTCCTGGCTCCTAGGCT
 CTTCCCTCCTCTCACTGGTTTCCACCTCCTCCCTCCCTTGTGGTGAATCTGAATTACTGTG
 GTGATATATATTGTATTATCTCTTCTTGTGGTGAATCTGAATTACTGTG
 GGATGTAAGTTCAAATAAGCCTTGCAAGATAA

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTAAACCAGCGCAGTCCTCCGTGCGTCCC GCCGCTGCCCTCACTCCC GGCCAGGATGG
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTTCTGGCCCTGC GGTG
CTCACAGACGATGTTCCACAGGAGCCC GTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCCGTGGACACC GGTC
CAGCCCCCACC GTCGGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGT CGCTGGGCCCGCGCTATCGCGGCCATCGT GATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGCGCTGAGAAAGTTTCTGCCTCCTGAAGCGAATAAA
GGGGCCCGGCCGGCCGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCGTTGGTGGTGC CGCGCTGAAGGGTGTGGCGAGCAGCGTCGGTGGCCGGCG
 CGGGCCGGGACGGGC**ATG**CCCTGCTGCTGCGCTGGTGTGCCTGACGGCGGCGCTGGCCA
 CGGCTGTCTGC ACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
 ACTTCAAGTCCTGGTGGGTGGCGACATCCCCGTGTCAAGGGCGCTGCTCACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCATCCCCGCAAGATCACCCGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAAGATGATGGATCAGCTGTACCAAGGGAAAGATGTACTTCC
 CCGGGTATTCCCCAACGAGCTGC GAAACATCTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGAGGAGGGCAGCTCTCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCC
 CCAGAGGC GCTGGAGTGTGCCCCCTCCGGGAGGCTCCATCTCACGCTGGG
 GTCAACCTGGGACCCCTTCCCTCCGGGCGATGGACACACATACATGAAAACCAGGCCGCAT
 CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACA ACTGCACAG
 ACTCGCACGTGCCCTGCTTGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGCTCCAGGCTCTCCTGGAGGGGGCTCCCCGCTTCCAC
 CTGGCTGT CATCGGGTAGGGCGGGCGTGGTTCAAGGGCGCACCACCTCCAAGCCTGTGT
 CCCACAGGTCCCTGGCGCAGTGGAA GTCAGCTGTCCAGGGCCTCTGAACACTACATAAAAC
 TGGCACAAGTAAGTCCCCTCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGT
 GGTGAGTATGTGTGGGCACAGGCTGGCTCCCTCAGCTCCCACGT CCTAGAGGGCTCCGA
 GGAGGTGGAACCTCAACCCAGCTCGCGCAGGAGGGCTGCAGTCCTTCTCCCTCAAAG
 GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTCTAAAGGGTCCCCATAGGGTCTGGTCC
 ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTCCCTACGATGGTTAGGGTGC
 ATGGAGGGGCTGACTGCCACATTGCCTTCAGACAGGACACGAGCATGAGGTAAAGGCCGC
 CCTGACCTGGACTTCAGGGGAGGGGTAAAGGGAGAGAGGGAGGGGGCTAGGGGTC
 AGATCAGTGGGGCACTGCAGGTGGGCTCTCCCTACCTGGACACCTGCTGGATGT
 CACTCTGCAACCACACCCATGTGGTGGTTCATGAACAGACCACGCTCCTCTGC
 CCTGGACACACAGGCCACCCGGCTTGTGAGTGACCCAGAGAAGGGAGGC
 CCTGGGAGAAGAGGCCACACAGGCCACCCGGCTGCACACCCCTCGGACATCCCAGGC
 ACGAGGGTGTGAGTGTGGGACACATAGGACCACACGTCCCAGCTGGGAGGGAGAGGC
 GGGGCCAGGGAGGGAGGCAGGGGTGGGGACATGGAGAGCTGAGGCAGCCTCGT
 CCTGGCAGCCTGGTATGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGG
 GACCTTGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGG
 GCCTGCCAGGGCAAC
 GTGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGCACTCTGGAGCTGG
 GCTGCTGC
 CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCAGGGCAGGG
 GAGGGAGGGAATGGGGTGGCTGTGCGCAGCATTAGCAGCCTGGCAG
 GTGAGCTGCGAGAGCTGCGGGAGGGAGGGAGGGAGGGAGGGAGGG
 TGTGATTAAAGTCCCTGATGTTCTC

FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMK
ELHLAIAPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP
```

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCGTCCAGGTTCATGTCCTCTTATTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTGCTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCCAGGATTAGAAATACCAGCAGTGCCACTCCA
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCAATTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAAACATCACTGGAACACCATCTGCCTTTGCCTGGTAGACAATGAACAACTG
 AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCAACAGCG
 CAACAGCCTCCACATGGTGACAGAGTACAACCTGTGACTGTGATTGGTTATTCAACAGCG
 TAATTAGATTCATCTCCTCTGATAATGAACAAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTTCCAGGGGAAGATTCTCTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTCAAACTAAAGGAGTCTCAACTGCCAG
 CTTGGCAATTACCAAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTCC
 GTAGAGCATGTGCAAAACTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTTCTCCTTGGAACTACATATGCC
 AAGTATCTACTTATGCAAAGTAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACACACACACACGCACGTGCACACACGCACGCACGCGTGCACAC
 ACACACGCGCACACACACACAGAGCTCATTCTGTCTAAAATCTGTTTCT
 TTCTCCTCTTTAAATTCTATCCTCACTCCCTATCCAATTCTCTTATCGTGCATT
 CATACTCTGTAAGCCCACCTGTAACACACACTAGATCAAGGCTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGCTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTCATAAGCACATGTCCGTCTGACTCAGGATAAAAACCAAAGG
 ATGGTTTAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTGGTTAGCATCTCCAACCTCC
 TATGTAATCAACAAACCTGCATAATAAATAAAAGGCAATCATGTTATA

FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLLFLLTCELAAEVAEEVEKSSDGPAGAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSFGISTDSEVLTHYNITGNTICLFRLVVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVIGLFNSVIQIHLLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCCGCGCTGGGACCGGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGGCGCGGGTG
 GCGGAGAGATCAGAACCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGCTCAGG
 GACGCGGCAGGGCGGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGGAGCCGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCTGGCGGGCGCTTGG
 GCTCTGACAGCTGGAGTATCAGCCTTGAAGTATACGCCAAAGAAATCTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCGACACTACTGTGTCGTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGATTATCCACCATTAAAGACAGAACATCAGCTGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCACATAGAAAATATGCAGTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTGTCCAGCCTGGACACATTAGGCTCTA
 TGTCGTAGAAAAAGAGAATTGCCTGTGTTCCAGTTGGTAGTGGTGGCATAGTTACTG
 CTGTGGCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCCTATAGAAGGAAA
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTGTCAACCAGTTAACAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGCTTGTAAAGAGTCTGCCCTCTGGATCTCACC
 AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGGTATGCGGATATCCGAAAGAAT**TAA**GAGAACATACCTAGAACATATC
 CTCAGCAAGAAACAAACCAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTACTCACAGAGGGAGAGAAAGATGTG
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGCTGTTTGACTTTCTTTC
 AGGTCAATTACAATTGGGAGATTCAAGAAACATTCCCTTCACCATCATTAGAAATGGTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGCCCTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTACAGTACAGTACATTATTGTCTGCCGCTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTGAGAAGTTTTGAAGTTTTCTCACT
 AAAATATGGGCAATTGTTAGCCTACATGTTGTAGACTTACTTAAGTTGCACCCCTG
 AAATGTGTCATATCAATTCTGGATTCAATAGCAAGATTAGCAAAGGATAATGCCGAAG
 GTCACCTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTGCTT
 GAGAACTTTGTAAACGTGGAGAGTAAAAGTATCGGTTTA

FIGURE 212

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAALGILLTAGVSALLEVYTPKEIFVANGTQGKLTCFKS
TSTTGGLTSVWSFQPEGADTTVSFFHYSQQVYLGNYPFFKDRISWAGDLDKKDASINEN
MQFIHNNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVVVGIVTAVVLGLTLLISM
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC **ATG**TACCGGCTCCTGTCAGCAGTGACTGCCGGCTGCCGCC
 CCCGGGGCTTGGCTCAAGCTGGGACGACGCCGGTCCATCAGCGCCGCCGGCTGCCGCC
 TCTCGGCCACGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGCCGCC
 TGGCAGGTGGCTGAGGGCGCGCCCCGGCGCAGTCCCCCGCGCCCCGACCTGAGGCG
 TCGCCTCTGGCGAGCCACAGGAGCAGTCCCTGCCCGTGGCTCCGAGACCCGGC
 GCCGCCCTGCTCCAGGTGCTCGCCAGGCCATCGAGAGCAGCCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGCGCACCGGCATAGTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTAGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAGTCTCACCATGGTGTCTGCCAAATTGTGGAAAG
 CAGGGAAACTGGATCTGATATTCCAGTACAACATTATGTTCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTCTGTACAACAAGATTACTGATTCCATTAAAGCCTGAAGATGA
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAACGCTTGAAGATGA
 TGAAAGAGAATGTTGCAATTGAGCAAGAAAAGAAGGCAAAAGTAATGAAAAGAATGATT
 ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTGAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT
 CCCTAACGATTATTAAAAATGATCCTTGTCTCAACCTGGTAGTCAGTTTGATTCA
 ACTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTCAGGATGTAATATTGGA
 CTATATGCAGAAAATATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAACGAGC
 CAGTGATTACAATAGAGCAAGG**TAA**ATGAATACTCTGCTGTCTAGCTATATCGCATIC
 TTAACACTATTATTAAATTAAAAGTCAAATTCTTGTCTTCCATTCAAAATCAACCTGC
 CACATTGGGAGCTTCTACATGTCTGTCTCATCTGTAAAGTGAAGGAAGTAAAACA
 TGTTTATAAAGTAAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGIASSCGRRGVHQAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPPDEASPLAEPPEQSLAPWSPQTAPPSCRCFARAIESSRDLLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLSLTVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKGKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTVQEENEPVIYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACCGTACGTAAGCTCGGAATTGGCTCG
 AGGCTGGTGGAAAGAACCCGAG**ATG**GCAGCAGCCAGCGCTGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCCGGGCAGCGGCTGCCGGGCCGGACT
 GGTGCGCGAGGGCTGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGCTGCT
 GCTGGAGCACTCATTGAGATCGATGACAGTGCCAACCTCCGAAGCGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGCAGCTCAGCGAGGAGGAGCGGGC
 CGACTCCGGATGTGGCAGCCCTGAATGCCCTGTACCGGGTCCGGATCCAAGGGCACCCGG
 GGCCCTGGATGCCCTGGAAGCTGGCTATGTCTCCTCCTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTCGGACCAGCTGACCTGCACGTGGATGTGGCGGCAACGTGGTGGC
 GTGTCGGTGGTACGCACCCCGGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGG
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
 TCCTTCTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCCTCATGATGTCAGG
 AGCGCCAGACACCGGGGCCAGGGTGGGGTGGGGGTGGGTGGTGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTAAAAACATCGACGATACTGAAATGTG
 TGAACGTTTAAAAGCTACAGCTCCAGCAGCCAAAGCAACTGTTGTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCACTGCTCACTGATACTGTTATTCAAACCCAAG
 GAATGGCTGTCCCCATCCTCATGTGGCTGTGGAGCTCAGCTGTGTGGCAGTTAT
 TAAACTGTCAGATCGACACGCAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSARGSGCRAVTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSSLWNQQDGTLSQRQLSEEERGRLRDVAALNGLYRVRIPRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEOKSFFAKYWMYIIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGSGLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

1000 1500 2000 2500 3000 3500 4000 4500 5000

GGAGCGCTGCTGGAACCGAGCCGGAGCCGGAGCCACAGCAGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCCGCAGACCAGGGCAGCAGGTGTCCTGGGGCTGGACC
ATGCTGGTGACTGCCTACCTGCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAACT
 GTCAAGATGCCGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTATGTCTG
 TGGCCTGCCTCTACAGTCCTCTTGGCTAGTGGCCTCCTCCCTGTGGATTGGCTGGTC
 GCAAGAATTCTTGTGTCCCTTCTCCCTGACTTACTCACTATGCTGCTAACCAAACTCT
 CAAGACTACTTGTGCTGCTAGTGGGGCGAGCACTGGTGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTCCCTGCTGAGT
 GGATCCCAGCTACCTTGCTCGAGCTGCCTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGGCCCTTGTGGCTGC
 CATCCCTCTGGCTCTGGCAGGGCCTGGCCCTCGAAACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCTGCGAACGCCGC
 GTGCTGCTGCTGGCACCATACAAGCTCTATTGAGAGTGTATCTCATCTTGTCTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGCATTATCTCTCAGCTTCATGG
 CAGCCAGCCTGCTGGCTCTCCCTGTACCGTATGCCACCTCCAAGAGGTACCACCTCAG
 CCCATGCACCTGCTGTCCCTGCTGTGCTCATCGTCGTTCTCTCTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTCCCAGCATGAGCTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTCCGGTACCTCTGCACTCACTGGCTGCCTAGGGCT
 CCTTGTCCCTCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTCAGCATTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGACTCTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTCACCTACTGAGGAGCCATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTGAATTCCAGCTATCCGGATTGTACAGATCTCTGT
 GACTGACTTTGTGACTGTCCTGTGGTTCTCCTGCCATTGCTTGTGTTGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTCCCTCTGTGTTACTCCCATTAGAAA
 ATAAACACTTTAAATGATCAAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARA_AFWNHVLA
VAEEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCA
GGLRCLLSDRRVLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGII
FSSFMAASLLGSSLYRIATSKRYHLP
PMHLLSLAVLIVVFSLFMLTFSTSPGQESP
VESFIAFLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVM
VMALLAVVGLFTVV
RHDAELRVPSPTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGGGGCGAGAGGAAACGCGGCCGGCCGGCCGGCCCTGGAGATG
 GTCCCCGGCGCCGGCTGGTGTCTCGTGCCTGGCTCCCCGCGTGCCTGGCCCA
 CGGCTTCCGTATCCATGATTATTGTACTTCAGTGCTGAGTCCTGGGACATTGATA
 TCTTCACAGCCACACCTGCCAAGGACTTGGTGGTATCTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCAGGGAACTCAGAACGGTTCTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGTGTATCATCTGACAAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCCCTGCTCGG
 CCGAGACGGCTACATGATCCGCCCTCTGGAACAGCATGGCTGCCATGGGCCATCATT
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTGAGCTGCTGCAACC GCCCTGGACCTC
 TGGTAGAAGAGTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGAAAGGGAAACCC
 AGGAATTGCTACTTGGAAATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTGGCGTTGCTAGGCTGAAAGGGAAAGCCACACCCTGGCCTCCCTCCCCAGG
 GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCAGGGCTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
 CACCTGGCTCCAGCCTCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTG
 AGTGGTTAAAGAGCTGGTGTGGGACTCAATAAACCTCACTGACTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAA

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

.....

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
AGGCCAACCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTATGACCACC
TGAAGACCCAGGGTGCAGCATCTACAAGGACAACAACAAAGCAGCATACTGTATGGAT
TTATCTCAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC
CGAATAAAAAGCTATTACTAWTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGC
HCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVF
NVIYLENEDSE
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGCCAGGAGAGTATAAAGGCATGTGGAG
GGTCCCCGGCACACCAGACGCCAGTCACAGGCAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTGCCCTCCTGGGGGCCACCTGGCAGGAAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTCCTGGTGAAAAGTGTCCAGGTGAAACTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTAGGTGGAAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTGTGCGCTTCCAAGCTTCCTCCGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTCTATTGGAGCTTGATGCCAGATCTCCTGCCTACCCCAGCCAAG
AGGGCAGGTGCTGGTGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCGAGTTAACATCTCACATACTC
AGCAAACTCACCGTGGTCGC**TAG**GGTGGGTATGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLKVSVQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:

amino acids 1-22

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCACGGAACTGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAATAACATCATGTTTCGATAAGAAGAAATTGTAGGATCCAGTT
 TTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTGATGTTGCTGCGAATCGGGTGTGGGATT
 TATTTGTTCTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGTCCAATTTCCTGGTGTAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGCTGTCACTGCAACTGGCCCCTAACGCAAAGCAGCTAACGGACGACCTTGAA
 CAATACAAAGG**A**TGGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTACTGACAATGCTTCTGCCAACGAGGATGCCCTAACGGCTG
 TAGGTGTGAAGGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTGTCCTCGCTATAACAGCCTCAAAAACCTTAAGTATAAT
 CAATTAAAGGGCTAACCGACTCACCTGGCTATAACCTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTAATGGAATACGCAACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTTCCTAACAAATACCTTCAGACCTGTGACAAATTACGGAACCTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAAACAGTTCGGGCTTGCGGAAGCTGCTGAGTT
 ACATTACGGCTAACCTCCCTGAGAACCATCCCTGTGCGAACATTCCAAGACTGCCGCAACC
 TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATGTCTTGCTGGC
 ATGATCAGACTCAAAGAACTCACCTGGAGCACAATCAATTTCAGCTAACCTGGCCCT
 TTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTGCACTGGAAATAAAATCAGTGTCAAG
 GACAGACCATGTCCTGGACCTGGAGCTCCTAACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCTGAACCTGGCTAACCTGG
 TTCCAACAAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACA
 TCAGTCTGCTGGGAATATGGGAATGCAAGCAGAACATTGCTGCCAGTCCCAAAGAGCTGCAAGG
 AAAAGTTAAAGGTCTAAGGGAGAACAAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCACTGGAGAACACTACAGCATCTGTGGAAAAGTACTACAGAGAGGT
 TTGATCTGCCAGGGCTCTCCAAAGCCGACGTTAACGCCAACGCTCCCCAGGCCAACGATGC
 GAGAGCAAACCCCTTGCCCCCGACGGTGGGAGCCACAGAGCCGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTCTGTCCG
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCACTGGAAAGCGGTACCCCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAACGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
 GACTCCCAGCACCCAGGAATTATGTAGATTATAACCCACCAACACGGAGACCAGCGAGA
 TGCTGCTGAATGGGACGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTTAAAGCTGGGAAATAAGTGGTGCTTTATTGAAACTC
 TGGTGAATCAAGGAAACGCGATGCCCTCCCTCCCTCTCCCTCACTTTGGTGG
 CAAGATCCTCCTGTCCGTTAGTGCATTCAATAACTGGTCAATTCTCCTCATACATA
 ATCAACCCATTGAAATTAAATACCAACAAATCAATGTGAAGCTTGAACCTCCGGTTAATATAA
 TACCTATTGTATAAGACCCCTTACTGATTCCATTAAATGTCGCAATTGTTAAAGATAAAACT
 TCTTCATAGGTAAAAAAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFN VIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG
CLGLSL RYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLFIGQEILDWSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELOGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCAACTATCCTAAGTTGACTGTCCTT
 TAAATATGTCAAGATCCAGACTTTCAGTGTACCTCAGCGATCTAACGATAAGGGATCTG
 TGTTGCCGCTATTCCAGTTGGTCTCGGACCTACCAGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCGCTGCTGGTTTGG
 TGGCAGCTCTCTGTGGAGCTGTGGCCTCTGCCCTCAGTGCTGGCTGAGGAGACCCGA
 ATTGATTCTCACAGGCGCACCATGGCAGTTTGCTGGAGACTGGACTCTATTATGG
 GACAGAAGCAGCTGTGAGTCCAAGTGTGGAAATTCACCTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCCGTCCATGTTGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCTGATTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTAGGAATAGTTATTCAGTTGGAAATGTCCAGAGATCTATTATCATA
 GTCTGAGGAAGGACAATTGACAAAAGAATGGATGGAAAAAATTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTGATGTGTCAGTGCTGTATCATACTTTATGCTACAC
 AACCAAATTAAATGCTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTAGGACTCCACTGCAGTATACAGCACACCATTCTGCTTAAACTCTTC
 CTAGCATGGGTCCATAAAATTATAATTAAACAATAGCCAAGCCGAGAATCCAACAT
 GTCCAGAACCGAGAACGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTGGAGTTGAAGGGTAAAGGATAAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAACAAGAGTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTCCC
 CTTTACAGTAATGAATGTGGCCTCCATAGTCAGTGTTCTCTGGAGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCTCGGCATAGGTATCTGTTCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTCAAGTGGCATTGGCAGTGGCCATCAGCAGGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTCAGCTGACAAATTGTTGAACAAAACAAT
 AACATCAATAGATATCTAAAAA

FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCVNNDQHNGWYIWILLLVLA
· ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGC GGAG TAAA ATCT CCACA AGCT GGG AACAA ACC TCGT CCA ACT CCC ACC CAC CGG C GT
 TTCT CCAG CT CGAT CT GGAGG CTGCT CGCCAGTGTGGACGCAGCTGACGCCGCTTATTA
 GCTCTCGCTCGCTCGCCCCGGCTCAGAACAGCTCCGTGGCGCGCAGCGTACGGAGAACGCC
 ACGCCAGCTCAGTTCTCTACTTTGGGAGAGAGAGAACAGTCAGATGCCCTTTAAACT
 CCCTCTCAAACATCTCCTGGGTGACTGAGTTAATAGAGTGGATAACAACCTGCTGAAG
 ATGAAGAATATAACAATATTGAGGATATTTTTCTTTTTCAAGTCTTGATTTGGC
 TTACCTCAAGTACCATTTCAAGTCAAGTCTGTTGTTGCTTCTCAGAA**ATG**TTTTA
 CAATCTCAAGAAAAATATGTCCCAGAAATTGAGTTACTGTTGTTGATTTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGCAAAGATATGTTAAAGCTCTAGCAGAGGAAATAAGA
 ACACAGTGGATGTCGAGAACGGTCTCTATGGCAGGATATGCGGACTGAAAAGAACAAATT
 GCTGTCCTCTGGATGACATTTGCAACGATTGGTGAAGCTGGAGAACAAAGTGACTATAT
 TGGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGAAATTGGTGCAGTAA
 CCACAAATAAAAGAACGAATGTCGGGCAGTATCAGA**TAG**CAGTTGAAAATCACCTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTACAATAAAAGCTCTACACATTTCAAGGAGTATGCTGGATTGAAAC
 TCTAATTCTGTACATAAAATTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG
 CTGTAATGTCCTTAAAGAGAATTGGTAACTTGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAAATCTTTGTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTC
 ATTTCTATAACACATTATTAAGTATATAACACGTTTTGGACAAGTGAAGAATGTTAA
 TCATTCTGTCAATTGTTCTCAATAGATGTAATGTTAGACTACGGCTATTGAAAAATGTG
 CTTATTGTAATATTGTTATTCCAATTATGAGCAGAGAACAGGAAATAATGTTGAAAA
 TAATGTTTGAAATCATGACCCAAAGAACATGTATTGACTATCCTCAGAATAACTGA
 AGGTTAATTATTGTATATTAAATTACACTTATAAGAGTATAATCTTGAAATGGTAG
 CAGCCACTGTCCATTACCTATCGAAACATTGGGCAATTAAACAGCATTAAAGT
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTGATGAGAGTAACAATA
 AAGTATTGATTTTCACATACATGAATGTTCAATTAAAGTTAATCCTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTATTCCATATTGGGTTAATTGCTTTATTATATTGGTC
 TAGGAGGAAGGGACTTGGAGAACGGAACTCTGAGGACTTGTAGCCAGGTGTATATAATAAA
 GGTACTTTGTGCTGCATTAAATTGCTTGAAAGTGTAAACATTATATTATAAGAGTATC
 CTTATGAAATTGAAATTGTTGATAACAGATGCATTAGATATTCAATTATATAATGGCAC
 TTAAATAAGAACATTAAATATAAAACTATGAAGATTGACTATCTTGAGGAAAAAGCT
 GTATATAGCACAGGGAACCCCTAATCTGGGTAAATTCTAGTATAAAACAAATTATACTTTAT
 TTAAATTCCCTGTAGCAAATCTAATTGCCACATGGTGCCTATATTCAAGTATT
 CTCTATAGTAATGCTTAAGTGCAGCTAGCTCTAGATTAGACTATATAAGAATTAGATAT
 TGTATTGTTGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTGTTAAAAA
 TAAATATGTGAAATATTGTTCATGAAAGACAGATTCCAAATCTCTCTCTCTGTGTA
 CTGTCACCTTATGTGAAGAAATTAAATTATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGЛИWGLMLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLDDILQRLVKLENKVVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 231

CGCGGCCGGGCGCCGGGTGAGCGTGCCGAGGC GGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCGTGGCCCCTGCTGCTGCTGGCGTGAGTGGGGCCAGACAACCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCA
 CTTGGACCTGTCCTCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGCCGGCT
 ACACGACGTTGGCTGGCAGTCAGCACAACTGCTCACAGCATCTCACCCACTGCC
 TTCTCCGCCTCGCTACCTGGAGTCGCTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTCACCAGCTACCCCTGAGCGACGTGAACCTAGCCACAACCAGCTCCGG
 AGGTCTCAGTGTCTGCCTCACGACGACAGTCAGGGCCGGCACTACACGTGGACCTCTCC
 CACAACCTCATTCAACCGCTCGTCCCCACCCACAGAGGGCCGGCTGCCTGCCACC
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC
 TGCGCTACCTGAGCCTGGATGGAAACCCCTAGCTGTCAATTGGTCCGGGTGCCCTCGCGGG
 CTGGGAGGCCTTACACACCTGTCTGGCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTCCGTGAGCTACCGGCTGCAGGTCTGGACCTGTCGGGCAACCCAAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTCGGGCACC
 AACCTGGTCCCCCTGCCTGAGGCGCTGCTCCTCACCTCCGGCACTGCAGAGCGTCAGCGT
 GGGCCAGGATGTGCGGTGCCGGCCCTGGTGCAGGGCACCTACCCCCGGAGGCCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCACC
 ATCTTG**TGA**CAAATGGTGTGGCCAGGGCACATAACAGACTGCTGTCTGGCTGCCCTAG
 GTCCCGAGTAACCTATGTTCAATGTGCCAACACCAGTGGGGAGCCCGAGGCCTATGTGGCA
 GCGTCACCACAGGAGTTGAGGCTTAGGAGAGGCTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTCACCCCTTGTCTACGTTGCTTCCCAAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAGACTCGGGTCCCCCTCCTGCTTCCCTCCCCACTTATCCCCAAGTGCCTCCCTCAT
 GCCTGGGCCGGCTGACCCGAATGGCAGAGGGTGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCCACTGGCTGAGTGTCCCTGGGCCATGGCCAGTCAGTCACTCAGGGCGAGTT
 TCTTTCTAACATAGCCCTTCTTGCCATGAGGCCATGAGGCCGCTTCATCCTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAGGAATTGCAAAGAATCAAGTCCACCCCTCATGTGAC
 AGATGGGAAACTGAGGCCTTGAGAAGGAAAAGGCTAATCTAAGTCCCTGCCAGTGGC
 ATGACTGGAGCACAGCCTCCTGCCCTCCAGCCCCAACATGCACTTTCTGTCTCCTCTA
 ATAAGCCCCACCCCTCCCCGCTGGCTCCCCCTGCTGCCCTGCCATTAGCACA
 GGAGTAGCAGCAGCACAGGCAAGAGCCTCACAAAGTGGACTCTGGCCTCTGACCAGCT
 GTGCGGCATGGCTAAGTCACTCTGCCCTCGGAGCCTCTGGAGCTTAGGGCACATTGGTT
 CCAGCCTAGCCAGTTCTCACCTGGGTTGGGTCCCCAGCATCCAGACTGGAAACCTACC
 CATTTCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
 TCTGGCTGGGATCTCAAGGGCCTCTGGATTCTAGTCCCCACTGCCCTGAGCACGACAGC
 CCTTCTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGCTGCCGACCCATGTCTATGC
 TCTACCCCAAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTCTAGTCTTCATTAA
 TAAAAGTTGTTGCCTTTAACGGAGTGTCACTTCAACCGGCCTCCCCAACCCCTGCTGGC
 CGGGGATGGAGACATGTCATTGTAAGCAGAAAAAGGTTGCATTGTTCACTTTGTAAT
 ATTGTCTGGGCCTGTGTTGGGTGTTGGGGAAAGCTGGGCATCAGTGGCACATGGGCATC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTGTCTTCCCCAACCTGCCTAGC
 CCATCATCTATCTAACCGGTCTTGATTAAACACTATAAAAGGTTAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDSLHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDPLRVLSDLGNPLAVIGPGAFAGLGGLTHLSSLASLQRLPELAPS
GFRELPGLQVLDSLGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVDV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCGATTCTCCCCAGTTCCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTCTGGAAAGGGGAGGCTAT**ATG**CGTCAATTCCCCA
 AAACAAGTTTGACATTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGCACTAACGGCGGAGCCAGGATGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTTAC
 GGGAGGCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTCAAGGCTAAGATGAAAGCC
 TCTAGTCTTGCCTCAGCCTCTCTGCTGCCTTATCTCTATGGACTCCTCCACTGG
 ACTGAAGACACTCAATTGGGAAGCTGTGATGCCACAAACCTTCAGGAAATACGAAATG
 GATTTCTGAGATACGGGCAGTGTGCAAGCCAAGATGGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTAAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTGCCAATTCTTTTACCATCAAGAAGGACCTCCGGCTCTCAT
 GCCCACATGACATGCCATTGTGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCTC
 TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGTGCTGCTGCTAAGAATATTGAGGT
 CAAGAGCTCCAGTCTCAATACCTGCAGAGGAGGCATGACCCAAACCCACCATCTCTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTGCATTACTGCTTCCATTGATGAT
 TGTCTTATGCATCCCCAATCTTAATTGAGACCATACTGTATAAGATTTGTAATATCTT
 TCTGCTATTGGATATATTATTAGTTAATATATTATTATTGCTATTAAATGTATT
 ATTTTTTACTGGACATGAAACTTAAAAAAATTACAGATTATTTATAACCTGACTAG
 ACCAGGTGATGTATTTTATACAGTAAAAAAAAACCTTGAAATTCTAGAAGAGTGGCT
 AGGGGGTTATTCATTGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA
 TATTGAAATTGAACCAATGACTACTTAGGATGGTTGTGGAATAAGTTTGATGTGGAATT
 GCACATCTACCTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCATAATTGTGTAT
 CTTCCAGCCAGGAATCCTACACGCCAGCATGTATTCTACAAATAAGTTCTTGCATA
 CCAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSIAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

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CCGTTATCGTCTTGCCTACTGCTGAATGTCGCCCCGGAGGAGGGAGGGCTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGCGCTACCGTGGC
 CGAGCTAGCAACCTTCCCCTGGATCTCACAAAAACTGACTCCAAATGCAAGGAGAACAG
 CTCTTGCTCGGTTGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTATTGCCAGTTTAGCCAATCCAAC TGACCTAGTGAAGGTTCAGATGCAAAT
 GGAAGGAAAAGGAAACTGGAAGGAAAACCATTGCGATTCGTGGTGTACATCATGCATTG
 CAAAAATCTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGCTGGTACCCAATATAACAA
 AGAGCAGCACTGGTGAATATGGGAGATTAAACCACTTATGACTCACGGTTATCAAGTTATGTTCTGGAC
 ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGGAACACCAGCCATGTCATCAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAGGAAGGGGACTTTGTATAATCATGACTGACTGCTTGATTCAAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTACCATCTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIEEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEH
YPLWKSIVGGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTYDTVKHYLVNLNTPLEDNIMTHGLSSLCGLVASICLGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACCGCTGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTCCTGCAGCGC
 GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGATAACAGCATTAAATGAAAAATTATGC
 TTAAGAAGTAAAATGGCAGGCTCCTAGATAATTTCGTTGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAAGAAATGCTGTGGCATCTGTTGTCGAGGTATATTGTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTACCTAACGCCAGAACAGTTGAACCAGCCTT
 TCACACATGTGGTGTATTCCACATTGGCTTCTTCATGATAAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT
 TTCATTGGTTCATGTTGATGTTGGTCACTTATTGCTCCATGTGGATTCTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTATCCGGGACTAGCTGTGTTTCAAAATGCACCTA
 TATTTTAGCACTCTGATCTACAAATTGGAAGAACCGAAGAGCTATGGACTGAGATCAC
 TTCTTAAGTCACATTTCCTTTGTTATTCTGTTAGATAGGTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTGTTCTTACATTATGTT
 TGAGTTTGAAATAGTTATGAAATTCTTATTTCATTGCAAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTATTCTGAGATTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTGTCATTAGAAGTAACCACTTTGT
 CTCTGGCTGGGCACGGTGGCTATGCCGTAACTCCAGCACTTGGGAGGCCGAGGCC
 CCGATTGCTTGAGGTCAAGTGTGAGACCAGCCTGCCAACATGGCAAACCCATCTACT
 AAAAATACAAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCAC
 TGCACCTAGCCTGGGGAGAAAGTGAAACTCCCTCTCAAAAAAGACCACTCTCAGTATC
 TCTGATTCTGAAGATGTACAAAAAATATGCTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTCAGCAAGTGTAACTTATTGGCTAAAGGTTTTGGTAAAGA
 AAAAATATTGTTCTATGTATTGAAGAAGTGTACTTTATATAATGATTTTAAATGCC
 AAAGGACTAGTTGAAAGCTTCTTAAAAAGAATTCCCTCTAATATGACTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVAVGILFFTGWWIMIDAAVVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALLFFSTLIYKFGRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGCAGGAGCAGCTGGCCA
 CTGGCGGCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCAGGGTGGT
 GGTCAGCTGGGTCAAGGACCTACGGCACCTGCTGGACCACCTCGCCTCTCCATCGAACAG
 GGAAGTGGAGCCTCGAGCCCTGGTGGAAAGCTGACCCAAAGCCACCCCTCACCTGGACAG
GATGAGAGTGTCAAGGTGTGCTCGCCTCGGCCCTCATCTTGCCATAGTCACGACATGGA
 TGTATTTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACACTTTGCGTTAAAATCTGCAGTGGGCCAACGTCGTGGCCCTACTATGT
 GCTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGCAGAGCCTAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGACAGAAGGCATTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACTGGTGTGGTGG
 CCTCCTACGACGATCCAGGGACAAATGAACGATGAAAGCAGGAAACTCTCTGACTTG
 GGGAGTCCTACGCAAACAACTGGCTTCCGGACAGCTGGTCTTCATAGGAGCCAAGA
 CCTCAGGGTAAAAGCCCCTTGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATT**TAGGGTGGC**
 TGTGGCTCTCCTCAGCCAGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGCTGAGGAGGAGCAGGGGTGCTGCGTGGAAAGGTGCTGCAGGTCTTGCACGC
 TGTGTCGCGCCTCTCCTCGAACAGAACCCCTCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGCTTCTGGAACCAGCTGTCTGGAGAGAATGGGGTGTTCGTCAGGG
 ACTGCTGACGGCTGGCCTGAGGAAGGACAAACTGCCAGACTTGAGCCAAATTAAATTAA
 TTTTGCTGGTTTGAAAAAAAAAAAAAA

FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLALIFAIVTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNNTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF
```

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTGGGAT
 CCAGAAACCCATGATAACCTACTGAACACCGAATCCCCTGGAAGGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCAGTCCC
 CTGCACCCCTCCTGGGACACT**ATG**TTGTTCTCCGCCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGCCA
 GCCTCTTACCCCTGAGTGTGGAAACAATGCCAGTCGCCATCGATATTGACAGACAGTGT
 GACATTGACCTGATTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
 CTTGGACCTGCACAACAATGCCACACAGTGCAACTCTCTGCCCTTACCCGTATCTG
 GGTGGACTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGTGAGAAAGGATC
 CCCAGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCTGGCT
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAACAGCTCAGTGCTCCCTCAACCTAACAGAG
 AGCTGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATGGCTCGCTCACAACTCCCCCT
 TGCTACCAGAGTGTGCTGGACAGTTTTATAGAAGGTCCAGATTCAATGGAACACAGCT
 GGAAAAGCTTCAGGGACATTGTTCTCCACAGAACAGAGGAGCCCTTAAGCTCTGGTACAGA
 ACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGCTTCTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTTAGGAATCTGGTTGGCTGTCTG
 CCTTCTCCTGGCTTTATTCATTGCTAGAAAGATTGGAAGAACAGGGCTGGAAAACGAA
 AGAGTGTGGTCTCACCTCAGCACAGCCACGACTGAGGCA**TAA**ATTCTCTCAGATACCA
 TGGATGTGGATGACTCCCTCATGCCTATCAGGAAGCCTCTAAATGGGTGAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACACTGCAGAGCCTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTTGCAGGG
 GAAGTTGGATATACCCCAAAGTCCTCTACCCCTCACTTTATGGCCCTTCCCTAGATA
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTGATCAATA
 TATTTGGAAATTAAAGTTCTGACTTT

FIGURE 242

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLPDLHLLNPAAGMTPGTQTHPLTLGGILNVQQQLHPHVLPIFVTQLGAQGTILSSEE
LPQIIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCAGCATTGATGCAGCCTGCAGCGGGCTCGGAGCGCGCG
 GAGCCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCCTGCCCG
 GCAGCCGGGAGCC **ATGCGACCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCCTGCCCG**
 TGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTCGGCTGGTCGAGACGGGAGCCCTGGGGCAATGTTATTCCGGGTACACCTG
 GGATCCCAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAG
 GAGTCCTGGACACCCAACCTACAAGCAGTGTTCATGGAGTTCATGATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGTACATTACAAAGATGCCTCAAATAGTCCTAAGAGTTTGT
 TCAGTGGCTCACTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTCACATTC
 AATGGAGCTGAATGTTCAAGGACCTCTCCCATTGAAGCTATAATTATTGGACCAAGGAAG
 CCCTGAAATGAATTCAACAATTAAATTATTCATCGCACTTCTCTGTGGAAGGACTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGGTGGCAATTGTTAGATTACCCAAAA
 GGAGATGCTTCTACTGGATGGAATTCAAGTTCTCGCATCATTATTGAAGAACTACCCAAA **TA**
AATGCTTAATTTCATTGCTACCTCTTTTATTATGCCTGGAATGGTCACTTAAAT
 GACATTAAATAAGTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTACAGA
 CCAAAGTGTGATTCACACTGTTTAAATCTAGCATTATTCAATTGCTTCAATCAAAAGT
 GGTTCAATATTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATTCTCTAACCTA
 TAATTGGAATATTGTTGGTCTTTGTTCTTAGTATAGCATTAAAAAAATA
 TAAAAGCTACCAATCTTGTACAATTGTAATGTTAAGAATTTTTATCTGTTAAAT
 AAAAATTATTCACCAACA

FIGURE 246

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217